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OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:57:18 ; Search time 363 Seconds

(without alignments)  
1475.762 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133  
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Scoring table: IDENTITY\_NUC  
Gpop 10.0 , Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:\*

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2: /SIDS5/ptodata/1/pubpna/US08\_NEW\_PUB.seq: \*  
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11: /SIDS5/ptodata/1/pubpna/US11\_NEW\_PUB.seq: \*  
12: /SIDS5/ptodata/1/pubpna/US11\_NEW\_PUB.seq: \*  
13: /SIDS5/ptodata/1/pubpna/US11\_NEW\_PUB.seq: \*  
14: /SIDS5/ptodata/1/pubpna/US11\_NEW\_PUB.seq: \*  
15: /SIDS5/ptodata/1/pubpna/US06\_NEW\_PUB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Match Length DB ID Description

RESULT 1  
US-10-527-048-14

; Sequence 14, Application US/10527048

; Publication No. US200600267041

; GENERAL INFORMATION:

; APPLICANT: Center for Genetic Engineering and Biotechnology

; TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.

; FILE REFERENCE: Vector for plastid transformation

; CURRENT APPLICATION NUMBER: US/10/527,048

; CURRENT FILING DATE: 2005-03-07

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO: 14

; LENGTH: 176

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA

; OTHER INFORMATION: fragment codifying for the promoter region of the plastid 16S

; OTHER INFORMATION: ribosomal RNA (Prm1), with added restriction sites.

US-10-527-048-14

Query Match 91.7%; Score 122; DB 9; Length 176;

Best Local Similarity 99.3%; Pred. No. 8.1e-31; Indels 1; Gaps 1;

Matches 133; Conservative 0; Mismatches 0;

Qy 1 GCTCCCCCGCCGTCGTCAATGAGAATGGATAAGAGCTCGTGGATGACGTGAGGG 60

Dy 16 GCTCCCCCGCCGTCGTCAATGAGAATGGATAAGAGCTCGTGGATGACGTGAGGG 75

Qy 61 CAGGGATGGCTATA-TTCYGGAGCGAACTCCCGGGCGATACGAAGAGCCTGATGATCAGT 119

Dy 76 CAGGGATGGCTATA-TTCYGGAGCGAACTCCCGGGCGATACGAAGAGCCTGATGATCAGT 135

## ALIGNMENTS

C 19 29.4 22.1 9136 14 US-11-136-527-3808 Sequence 3808, AP  
C 20 29 21.8 7479 14 US-11-136-527-3308 Sequence 3308, AP  
C 21 27.6 20.8 507 6 US-09-925-065A-132559 Sequence 132559,  
C 22 27.6 20.8 507 6 US-09-925-065A-132559 Sequence 132559,  
C 23 27.6 20.8 507 6 US-09-925-065A-132560 Sequence 132560,  
C 24 27.6 20.8 518 9 US-10-301-480-2842178 Sequence 842179,  
C 25 27.6 20.8 518 10 US-10-301-480-613693 Sequence 842180,  
C 26 27.6 20.8 526 10 US-10-301-480-228769 Sequence 228769,  
C 27 27.6 20.8 526 10 US-10-301-480-228770 Sequence 228770,  
C 28 27.6 20.8 526 10 US-10-301-480-228771 Sequence 228771,  
C 29 27.6 20.8 526 10 US-10-301-480-842178 Sequence 842178,  
C 30 27.6 20.8 526 10 US-10-301-480-842179 Sequence 842179,  
C 31 27.6 20.8 526 10 US-09-925-065A-698990 Sequence 698990,  
C 32 27.6 20.8 640 6 US-09-925-065A-512338 Sequence 512338,  
C 33 27.4 20.6 61487 14 US-11-124-3678-5103 Sequence 5103, AP  
C 34 27.4 20.6 634 9 US-10-301-480-26304 Sequence 26304, A  
C 35 27.2 20.5 634 9 US-10-301-480-26304 Sequence 26305, A  
C 36 27.2 20.5 634 10 US-10-301-480-639713 Sequence 639713,  
C 37 27.2 20.5 634 10 US-10-301-480-639714 Sequence 639714,  
C 38 27.2 20.5 533 6 US-09-925-065A-13188 Sequence 13188, A  
C 39 27.2 20.3 533 9 US-10-301-480-114425 Sequence 114425,  
C 40 27.2 20.3 533 10 US-10-301-480-727834 Sequence 727834,  
C 41 27.2 20.3 568 6 US-09-925-065A-619601 Sequence 619601,  
C 42 27.2 20.3 985 14 US-11-136-527-1708 Sequence 1708, AP  
C 43 27.2 20.3 985 14 US-11-136-527-5804 Sequence 5804, AP  
C 44 27.2 20.3 1694969 7 US-10-505-454-1690 Sequence 1690, AP

RESULT 2  
US-10-527-048-15

Sequence 15, Application US/10527048  
Publication No. US20060026704A1

GENERAL INFORMATION:

APPLICANT: Center for Genetic Engineering and Biotechnology.  
TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.  
FILE REFERENCE: Vector for plastid transformation

CURRENT APPLICATION NUMBER: US10/527,048  
CURRENT FILING DATE: 2005-03-07  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 15  
LENGTH: 5834

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA  
OTHER INFORMATION: fragment from the vector pVTPA between the rice atpB and  
OTHER INFORMATION: tobacco rbcL borders.

US-10-527-048-15

Query Match 91.7%; Score 122; DB 9; Length 5834;  
Best Local Similarity 99.3%; Pred. No. 1.5e-30;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGGCGGTCAATGAGATCAAGGGCGTGGAGTCAGCCTGGGGGG 60  
Db 1918 GCTCCCCCGGCGGTCAATGAGATCAAGGGCGTGGAGTCAGCCTGGGGGG 1977

QY 61 CAGGGATGGCTATA-TTCGGGAGGAACCTCGGGGAATACGAGGCGCTGGGGGG 119  
Db 1978 CAGGGATGGCTATA-TTCGGGAGGAACCTCGGGGAATACGAGGCGCTGGGGGG 2037

QY 120 TGTAGGGAGGATT 133  
Db 2038 TGTAGGGAGGATT 2051

RESU . 3

US-10-527-048-25

; Sequence 25, Application US/10527048  
; Publication No. US20060026704A1

GENERAL INFORMATION:

APPLICANT: Center for Genetic Engineering and Biotechnology.  
TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.  
FILE REFERENCE: Vector for plastid transformation

CURRENT APPLICATION NUMBER: US10/527,048  
CURRENT FILING DATE: 2005-03-07  
NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 25  
LENGTH: 6465

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA  
OTHER INFORMATION: fragment from the vector pVTPA-Bar between the rice atpB and  
OTHER INFORMATION: tobacco rbcL borders.

US-10-527-048-25

Query Match 91.7%; Score 122; DB 9; Length 6465;  
Best Local Similarity 99.3%; Pred. No. 1.5e-30;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGGCGGTCAATGAGATCAAGGGCGTGGAGTCAGCCTGGGGGG 60  
Db 1918 GCTCCCCCGGCGGTCAATGAGATCAAGGGCGTGGAGTCAGCCTGGGGGG 1977

QY 61 CAGGGATGGCTATA-TTCGGGAGGAACCTCGGGGAATACGAGGCGCTGGGGGG 119  
Db 1978 CAGGGATGGCTATA-TTCGGGAGGAACCTCGGGGAATACGAGGCGCTGGGGGG 2037

QY 120 TGTAGGGAGGATT 133

RESU . 3

US-10-527-048-25

; Sequence 25, Application US/10527048  
; Publication No. US20060026704A1

GENERAL INFORMATION:

APPLICANT: Center for Genetic Engineering and Biotechnology.  
TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.  
FILE REFERENCE: Vector for plastid transformation

CURRENT APPLICATION NUMBER: US10/527,048  
CURRENT FILING DATE: 2005-03-07  
NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 25  
LENGTH: 6465

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA  
OTHER INFORMATION: fragment from the vector pVTPA-Bar between the rice atpB and  
OTHER INFORMATION: tobacco rbcL borders.

US-10-527-048-25

RESULT 4

US-10-527-048-22

; Sequence 22, Application US/10527048  
; Publication No. US20060026704A1

GENERAL INFORMATION:

APPLICANT: Center for Genetic Engineering and Biotechnology.  
TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.  
FILE REFERENCE: Vector for plastid transformation

CURRENT APPLICATION NUMBER: US10/527,048  
CURRENT FILING DATE: 2005-03-07  
NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22  
LENGTH: 6659

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA  
OTHER INFORMATION: fragment from the vector pVTPA-aada between the rice atpB and  
OTHER INFORMATION: tobacco rbcL borders.

US-10-527-048-22

Query Match 91.7%; Score 122; DB 9; Length 6659;  
Best Local Similarity 99.3%; Pred. No. 1.5e-30;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGGCGGTCAATGAGATCAAGGGCGTGGAGTCAGCCTGGGGGG 60  
Db 1918 GCTCCCCCGGCGGTCAATGAGATCAAGGGCGTGGAGTCAGCCTGGGGGG 1977

QY 61 CAGGGATGGCTATA-TTCGGGAGGAACCTCGGGGAATACGAGGCGCTGGGGGG 119  
Db 1978 CAGGGATGGCTATA-TTCGGGAGGAACCTCGGGGAATACGAGGCGCTGGGGGG 2037

QY 120 TGTAGGGAGGATT 133  
Db 2038 TGTAGGGAGGATT 2051

RESU . 3

US-10-527-048-24

RESULT 5

US-10-527-048-24

; Sequence 24, Application US/10527048  
; Publication No. US20060026704A1

GENERAL INFORMATION:

APPLICANT: Center for Genetic Engineering and Biotechnology.  
TITLE OF INVENTION: VECTOR FOR PRODUCTION OF ANGIOSPERM TRANSPLASTOMIC PLANTS.  
FILE REFERENCE: Vector for plastid transformation

CURRENT APPLICATION NUMBER: US10/527,048  
CURRENT FILING DATE: 2005-03-07  
NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 24  
LENGTH: 7549

TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence of DNA  
OTHER INFORMATION: fragment from the vector pVTPA-HB-aada between the rice atpB and  
OTHER INFORMATION: tobacco rbcL borders.

US-10-527-048-24

Query Match 91.7%; Score 122; DB 9; Length 7549;  
Best Local Similarity 99.3%; Pred. No. 1.5e-30;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGGCGGTCAATGAGATCAAGGGCGTGGAGTCAGCCTGGGGGG 60  
Db 2808 GCTCCCCCGGCGGTCAATGAGATCAAGGGCGTGGAGTCAGCCTGGGGGG 2867

QY 61 CAGGGATGGCTATA-TTCGGGAGGAACCTCGGGGAATACGAGGCGCTGGGGGG 119



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; PRIORITY APPLICATION NUMBER: 6/0/393,651
; PRIORITY FILING DATE: 2002-07-03
; PRIORITY APPLICATION NUMBER: 6/0/393,428
; PRIORITY FILING DATE: 2002-07-03
; PRIORITY APPLICATION NUMBER: PCT/US2002/041503
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2
; LENGTH: 3119
; TYPE: DNA
; ORGANISM: ARTIFICIAL
; FEATURE:
; OTHER INFORMATION: gfp/BADH expression cassette
; US-11-190-122-2

Query Match 77.3%; Score 102.8; DB 11; Length 3119;
Best Local Similarity 90.3%; Pred. No. 3.2e-24;
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;
Qy 1 GCGGCCCCGGCGC3RGTCAATGAGAATGATGAGAGGCTCGTGGATTGACCTGAGGGG 60
Db 79 GCTTCCCCGGCGTGTCAATGAGAATGATGAGAGGCTCGTGGATTGACCTGAGGGG 138
Qy 61 CAGGGATGCTATA-TTCGGGGAGACTCCGGGAAATAGAGGGCTTGATGACT 119
Db 139 CAGGGATGCTATAATTCTGGAGCGAACTCCGGGGRATATGAGGCCATGGATAACAG 198
Qy 120 TGTAGGGAGGATT 133
Db 199 TTATGCCCTGGAAT 212

RESULT 9
US-11-004-399-377
; Sequence 377, Application US/1104399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; FILE REFERENCE: 2587/73166/RDK
; CURRENT FILING DATE: 2004-12-03
; PRIORITY FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 378
; LENGTH: 8082
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: pcVB
; NAME/KEY: CDS
; LOCATION: (1)..(8082)
; OTHER INFORMATION:
; US-11-004-399-378

Query Match 46.8%; Score 62.2; DB 11; Length 8082;
Best Local Similarity 73.2%; Pred. No. 1.2e-10;
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;
Qy 4 CCCCGCGCTGTCTCAATGAGAATGATGAGGCTCTGCAATGAGGTGGGGCGAG 63
Db 3326 CCCCCGCACGATCGACGGGATGGTTAGAGGGCTGTGGATGGTAGGTAG 3385
Qy 64 GATGGCTATA-TTCGGGGAGCACTCCGGGAAATACGAAGCGCTTGATACTGT 122
Db 3386 GCTTGCTATACTGCTGTGGAGACTCCAGGCTTAATACTGAAAGCGCTTCAA 3445
Qy 123 AGGGAGG 129
Db 3446 AGGGAGG 3452

RESULT 11
US-11-004-399-483
; Sequence 483, Application US/1104399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; FILE REFERENCE: 2587/73166/RDK
; CURRENT FILING DATE: 2004-12-03
; PRIORITY FILING NUMBER: US/11/004,399
; PRIORITY FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 483
; LENGTH: 8082

Query Match 46.8%; Score 62.2; DB 11; Length 8040;
Best Local Similarity 73.2%; Pred. No. 1.2e-10;
Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;
Qy 4 CCCCGCGCTGTCTCAATGAGAATGATGAGGCTCTGCAATGAGGTGGGGCGAG 63
Db 3284 CCCCCGCCACGATGACCTGAGAATGAGGCTCTGCAATGAGGTGGGGCGAG 3343
Qy 64 GGTGGCTATA-TTCGGGGAGCACTCCGGGAAATACGAAGCGCTTGAGTGT 122
Db 3344 GGTTGGCTATACTGCTGTGGCGAACCTCCAGGCTTAATACTGAAAGCGCTTCAA 3403
Qy 123 AGGGAGG 129

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TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: pcvb

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (2).. (8080)  
 OTHER INFORMATION:  
 US-11-004-399-483

Query Match 46.8%; Score 62.2; DB 11; Length 8082;  
 Best Local Similarity 73.2%; Pred. No. 1.2e-10;  
 Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCGCCGCGTCGTCAATGAGTGAAGGGCTCGTGGATTGACGTGAGGGCGAG 63  
 Db 3326 CCCCGCCGCGACATCGAGCAGGGATGATGAGAAGGGCTCGTGGATTGACGTGAGGGCGAG 3385

QY 64 GGATGGCTATA-TTCTGGAGGCGAACTCCGGCGATAACCGCTTGATACGTTG 122  
 Db 3386 GGTTGGCTATACTGCCTGGCGAACCTCCAGGCTATAATCTGAAGCGCTTGGAAAGTGT 3445

QY 123 AGGGAGG 129  
 Db 3446 AGGGAGG 3452

RESULT 12

US-11-004-399-605

; Sequence 605, Application US/1104399

; Publication No. US20060053516A1

; GENERAL INFORMATION:

; APPLICANT: Chye, Mee Lee

; APPLICANT: Li, Hong Ye

; APPLICANT: Ramalingam, Sathiskumar

; APPLICANT: Poon, Leo Litt Man

; APPLICANT: Peiris, Joseph Sriyal Malik

; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide Title of Invention: Sequences and Methods of Use Thereof For Immunization Against SARS-CoV

; FILE REFERENCE: 2587/73166/RDK

; CURRENT APPLICATION NUMBER: US/11/004, 399

; CURRENT FILING DATE: 2004-12-03

; PRIOR APPLICATION NUMBER: US 60/527, 637

; PRIOR FILING DATE: 2003-12-03

; NUMBER OF SEQ ID NOS: 4043

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 9348

TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: pcvb

NAME/KEY: CDS  
 LOCATION: (1).. (9348)

; OTHER INFORMATION:

US-11-004-399-1

Query Match 46.8%; Score 62.2; DB 11; Length 9348;  
 Best Local Similarity 73.2%; Pred. No. 1.2e-10;  
 Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 4 CCCCGCCGCGTCGTCAATGAGTGAAGGGCTCGTGGATTGACGTGAGGGCGAG 63  
 Db 4592 CCCCGCCGCGACATCGAGCAGGGATGATGAGAAGGGCTCGTGGATTGACGTGAGGGCGAG 4651

QY 64 GGATGGCTATA-TTCTGGAGGCGAACTCCGGCGATAACCGCTTGATACGTTG 122  
 Db 4652 GGTTGGCTATACTGCCTGGCGAACCTCCAGGCTATAATCTGAAGCGCTTGGAAAGTGT 4711

QY 123 AGGGAGG 129  
 Db 4712 AGGGAGG 4718

RESULT 14

US-11-004-399-113

; Sequence 113, Application US/1104399

; Publication No. US20060053516A1

; GENERAL INFORMATION:

; APPLICANT: Chye, Mee Lee

; APPLICANT: Li, Hong Ye

; APPLICANT: Ramalingam, Sathiskumar

; APPLICANT: Poon, Leo Litt Man

; APPLICANT: Peiris, Joseph Sriyal Malik

; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide Title of Invention: Sequences and Methods of Use Thereof For Immunization Against SARS-CoV

; FILE REFERENCE: 2587/73166/RDK

; CURRENT APPLICATION NUMBER: US/11/004, 399

; CURRENT FILING DATE: 2004-12-03

; PRIOR APPLICATION NUMBER: US 60/527, 637

; PRIOR FILING DATE: 2003-12-03

; NUMBER OF SEQ ID NOS: 4043

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 113

; LENGTH: 9348

TYPE: DNA  
 ORGANISM: Artificial Sequence

Search completed: April 18, 2006, 00:03:30  
Job time : 365 secs

; FEATURE: OTHER INFORMATION: pCV1  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2)..(3346)  
; OTHER INFORMATION:  
US-11-004-399-113

US-11-004-399-274  
 Sequence 274, Application US/11/004399  
 Publication No. US20060053516A1  
 GENERAL INFORMATION:  
 APPLICANT: Chye, Mee Lee  
 APPLICANT: Li, Hong Ye  
 APPLICANT: Ramalingam, Sathishkumar  
 APPLICANT: Poon, Leo Litt Man  
 APPLICANT: Peiris, Joseph Sriyal Malik  
 TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide Sequences and Methods of Use Thereof For Immunization Against SARS-CoV  
 TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against SARS-CoV  
 FILE REFERENCE: 2587 /73166.RDK  
 CURRENT APPLICATION NUMBER: US/11/004,399  
 CURRENT FILING DATE: 2004-12-03  
 PRIORITY APPLICATION NUMBER: US 60/527,637  
 PRIORITY FILING DATE: 2003-12-03  
 NUMBER OF SEQ ID NOS: 4043  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 274  
 LENGTH: 9348  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: pcv1  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (3)..(9347)  
 ; OTHER INFORMATION:  
 US-11-004-399-274

Query Match 46.8%; score 62.2; DB 11; Length 9348;  
 Best Local Similarity 73.2%; Pred. No. 1.2e-1; 33; Indels 1; Gaps 1;  
 Matches 93; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY	4	CCCCCGCGTCGTCAATGAGATGATAAGGGCTGTGGATGCGTGAGGGCAG	63
Db	4592	CCCCCGCCACGATGAGACGGGATGATAAGGGCTGTGGATGCGATAGGGTAG	4651
QY	64	GGATGGCTATA-TTCTGGAGGGAACTCCGGGAATAGCAGGGTTGGATACAGTGT	122
Db	4652	GCTTGGCTATACGTGCTGGAACTCCAGGCTTAATCTGAGACGGCTTGGAGGTGT	4711
QY	123	ACGGAGG 129	
Db	4712	AGGGAGG 4718	

Om nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:49:25 ; Search time 454 Seconds  
                   (without alignments)  
                   2422.527 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133

Sequence: gtcggccggcgctcggttcaaaaaaaaaaaaaatacagttgttagggaggatt 133

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqB, 413469005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
                   Maximum Match 100%  
                   Listing first 45 summaries

**Database :**

Published Applications NA\_Main:\*

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- 3: /cgn2\_6/prodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
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2	122	91	133	Sequence 32, Appl
3	122	91	7	US-10-660-716-2
4	121	91	7	US-10-660-716-3
5	119	89	8	US-10-673-207-26
6	119	89	7	US-10-673-207-4
7	107	80	5	US-10-673-207-25
8	102	8	119	US-10-681-813-6
9	102	8	7	US-10-695-514-3
10	102	8	233	US-10-737-251-38
11	102	8	7	US-10-737-251-34-63
12	102	8	7	US-10-737-251-41
13	102	8	77	US-10-680-824A-2
14	102	8	77	US-10-943-324A-19
15	96	72	3	US-10-680-824A-2
16	94	70	7	US-10-258-253-16
17	93	70	1	US-10-737-251-41
18	91	68	9	US-10-737-251-42
19	87	65	7	US-10-737-251-42
20	87	63	7	US-09-843-324A-2
21	83	63	0	US-10-737-251-3
22	83	63	9	US-10-737-251-43
23	83	62	9	US-10-460-716-1
			1993	US-10-460-716-1

**ALIGNMENTS**

RESULT 1

US-10-663-241-32

; Sequence 32, Application US/10663241  
     Publication No. US20040040058A1

; GENERAL INFORMATION:

; APPLICANT: Malig, Pal

; APPLICANT: Silhavy, Daniel

; APPLICANT: Sirman, Priya

; TITLE OF INVENTION: Plastid Promoters for Transgene

; TITLE OF INVENTION: Expression in the Plastids of Higher Plants

; FILE REFERENCE: Rut 97-0097

; CURRENT APPLICATION NUMBER: US/10/663, 241

; CURRENT FILING DATE: 2003-09-16

; PRIOR APPLICATION NUMBER: US/09/445, 283C

; PRIOR FILING DATE: 1999-12-03

; PRIOR APPLICATION NUMBER: PCT/US98/11437

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: 60/058, 670

; PRIOR FILING DATE: 1997-09-12

; PRIOR APPLICATION NUMBER: 60/048, 376

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ\_ID NO 32

; LENGTH: 133

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE: Other

; OTHER INFORMATION: Prin promoter

Query Match Score: 100.0%; Score: 133; DB: 7; Length: 133;  
     Best Local Similarity: 100.0%; Score: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Matches: 133; Conservative: 0;

Sequence 1, Appl

Sequence 2, Appl

Sequence 3, Appl

Sequence 4, Appl

Sequence 5, Appl

Sequence 6, Appl

Sequence 7, Appl

Sequence 8, Appl

Sequence 9, Appl

Sequence 10, Appl

Sequence 11, Appl

Sequence 12, Appl

Sequence 13, Appl

Sequence 14, Appl

Sequence 15, Appl

Sequence 16, Appl

Sequence 17, Appl

Sequence 18, Appl

Sequence 19, Appl

Sequence 20, Appl

Sequence 21, Appl

Sequence 22, Appl

Sequence 23, Appl

Sequence 24, Appl

Sequence 25, Appl

Sequence 26, Appl

Sequence 27, Appl

Sequence 28, Appl

Sequence 29, Appl

Sequence 30, Appl

Sequence 31, Appl

Sequence 32, Appl

Sequence 33, Appl

Sequence 34, Appl

Sequence 35, Appl

Sequence 36, Appl

Sequence 37, Appl

Sequence 38, Appl

Sequence 39, Appl

Sequence 40, Appl

Sequence 41, Appl

Sequence 42, Appl

Sequence 43, Appl

Sequence 44, Appl

Sequence 45, Appl

Sequence 46, Appl

Sequence 47, Appl

Sequence 48, Appl

Sequence 49, Appl

Sequence 50, Appl

Sequence 51, Appl

Sequence 52, Appl

Sequence 53, Appl

Sequence 54, Appl

Sequence 55, Appl

Sequence 56, Appl

Sequence 57, Appl

Sequence 58, Appl

Sequence 59, Appl

Sequence 60, Appl

Sequence 61, Appl

Sequence 62, Appl

Sequence 63, Appl

Sequence 64, Appl

Sequence 65, Appl

Sequence 66, Appl

Sequence 67, Appl

Sequence 68, Appl

Sequence 69, Appl

Sequence 70, Appl

Sequence 71, Appl

Sequence 72, Appl

Sequence 73, Appl

Sequence 74, Appl

Sequence 75, Appl

Sequence 76, Appl

Sequence 77, Appl

Sequence 78, Appl

Sequence 79, Appl

Sequence 80, Appl

Sequence 81, Appl

Sequence 82, Appl

Sequence 83, Appl

Sequence 84, Appl

Sequence 85, Appl

Sequence 86, Appl

Sequence 87, Appl

Sequence 88, Appl

Sequence 89, Appl

Sequence 90, Appl

Sequence 91, Appl

Sequence 92, Appl

Sequence 93, Appl

Sequence 94, Appl

Sequence 95, Appl

Sequence 96, Appl

Sequence 97, Appl

Sequence 98, Appl

Sequence 99, Appl

Sequence 100, Appl

Sequence 101, Appl

Sequence 102, Appl

Sequence 103, Appl

Sequence 104, Appl

Sequence 105, Appl

Sequence 106, Appl

Sequence 107, Appl

Sequence 108, Appl

Sequence 109, Appl

Sequence 110, Appl

Sequence 111, Appl

Sequence 112, Appl

Sequence 113, Appl

Sequence 114, Appl

Sequence 115, Appl

Sequence 116, Appl

Sequence 117, Appl

Sequence 118, Appl

Sequence 119, Appl

Sequence 120, Appl

Sequence 121, Appl

Sequence 122, Appl

Sequence 123, Appl

Sequence 124, Appl

Sequence 125, Appl

Sequence 126, Appl

Sequence 127, Appl

Sequence 128, Appl

Sequence 129, Appl

Sequence 130, Appl

Sequence 131, Appl

Sequence 132, Appl

Sequence 133, Appl

Sequence 134, Appl

Sequence 135, Appl

Sequence 136, Appl

Sequence 137, Appl

Sequence 138, Appl

Sequence 139, Appl

Sequence 140, Appl

Sequence 141, Appl

Sequence 142, Appl

Sequence 143, Appl

Sequence 144, Appl

Sequence 145, Appl

Sequence 146, Appl

Sequence 147, Appl

Sequence 148, Appl

Sequence 149, Appl

Sequence 150, Appl

Sequence 151, Appl

Sequence 152, Appl

Sequence 153, Appl

Sequence 154, Appl

Sequence 155, Appl

Sequence 156, Appl

Sequence 157, Appl

Sequence 158, Appl

Sequence 159, Appl

Sequence 160, Appl

Sequence 161, Appl

Sequence 162, Appl

Sequence 163, Appl

Sequence 164, Appl

Sequence 165, Appl

Sequence 166, Appl

Sequence 167, Appl

Sequence 168, Appl

Sequence 169, Appl

Sequence 170, Appl

Sequence 171, Appl

Sequence 172, Appl

Sequence 173, Appl

Sequence 174, Appl

Sequence 175, Appl

Sequence 176, Appl

Sequence 177, Appl

Sequence 178, Appl

Sequence 179, Appl

Sequence 180, Appl

Sequence 181, Appl

Sequence 182, Appl

Sequence 183, Appl

Sequence 184, Appl

Sequence 185, Appl

Sequence 186, Appl

Sequence 187, Appl

Sequence 188, Appl

Sequence 189, Appl

Sequence 190, Appl

Sequence 191, Appl

Sequence 192, Appl

Sequence 193, Appl

Sequence 194, Appl

Sequence 195, Appl

Sequence 196, Appl

Sequence 197, Appl

Sequence 198, Appl

Sequence 199, Appl

Sequence 200, Appl

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RESULT 2 ; FEATURE: OTHER INFORMATION: Synthetic construct
; US-10-460-716-2/C
; Sequence 2, Application US/10460716
; Publication No. US20030200568A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Skarjinskaia, Marina
; APPLICANT: Svab, Zora
; APPLICANT: Rutgers, The State University of New Jersey
; TITLE OF INVENTION: Plastid Transformation in Lesquerella
; FILE REFERENCE: Rut 0-0109CIP
; CURRENT APPLICATION NUMBER: US/10/460,716
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US/09/524,087A
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: PCT/US97/03444
; PRIOR FILING DATE: 1997-03-06
; PRIOR APPLICATION NUMBER: 60/102,716
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Nicotinum tobacum
; US-10-460-716-2

Query Match 91.7%; Score 122; DB 6; Length 1143;
Best Local Similarity 99.3%; Pred. No. 2. 8e-35; 0; Mismatches 0; Indels 1; Gaps 1;
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
; US-10-473-207-26
; Sequence 26, Application US/10473207
; Publication No. US20040163145A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Cornelle, Sylvie
; APPLICANT: Lutz, Kerry
; TITLE OF INVENTION: Integrases for the insertion of heterologous nucleic acids into the plastid genome
; FILE REFERENCE: 1594-RUT.01-091US
; CURRENT APPLICATION NUMBER: US/10/473,207
; PRIOR FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: PCT/US02/09537
; PRIOR FILING DATE: 2002-03-29
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 2145
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: plasmid fragment
; OTHER INFORMATION: plasmid fragment
; US-10-473-207-26

Query Match 91.0%; Score 121; DB 7; Length 2145;
Best Local Similarity 99.2%; Pred. No. 7. 7e-35; 0; Mismatches 0; Indels 1; Gaps 1;
Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
; US-10-473-207-4/C
; Sequence 4, Application US/10473207
; Publication No. US20040163145A1
; GENERAL INFORMATION:
; APPLICANT: Maliga, Pal
; APPLICANT: Skarjinskaia, Marina
; APPLICANT: Svab, Zora
; APPLICANT: Rutgers, The State University of New Jersey
; TITLE OF INVENTION: Plastid Transformation in Lesquerella
; TITLE OF INVENTION: Fendleria, an Oilseed Brassicaceae
; FILE REFERENCE: Rut 0-0109CIP
; CURRENT APPLICATION NUMBER: US/10/460,716
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US/09/524,087A
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: PCT/US97/03444
; PRIOR FILING DATE: 1997-03-06
; PRIOR APPLICATION NUMBER: 60/102,716
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1417
; TYPE: DNA
; ORGANISM: Artificial Sequence

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; TITLE OF INVENTION: Integrases for the insertion of heterologous nucleic acids into the plastid genome  
; FILE REFERENCE: 1594-RUT-01-091US  
; CURRENT APPLICATION NUMBER: US10/473,207  
; PRIORITY APPLICATION NUMBER: PCT/US02/09537  
; PRIORITY FILING DATE: 2002-03-29  
; PRIORITY APPLICATION NUMBER: 60/279615  
; PRIORITY FILING DATE: 2001-03-29  
; SEQ ID NO 4  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: vector insert  
; US-10-473-207-4

Query Match 89.8%; Score 119.4; DB 7; Length 1544;  
Best Local Similarity 98.5%; Pred. No. 2.9e-34; Mismatches 1; Indels 1; Gaps 1;  
Matches 131; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCCGCGTCGTCAATGAGAATGATGATAAGGGCTCGTGGATGACGTTGAGGGGG 60  
Db 1393 GCTCCCCCGCCGCGTCGTCAATGAGAATGATGATAAGGGCTCGTGGATGACGTTGAGGGGG 1334  
QY 61 CAGGGATGCATA-TTCGGGAGGAACTCCGGGCAATACGAGCCTTGAAATACAGT 119  
Db 1333 CAGGGATGCATA-TTCGGGAGGAACTCCGGGCAATACGAGCCTTGAAATACAGT 1274

QY 120 TCTAGGGAGGAT 132  
Db 1273 TGTAGGGAGGAT 1261

RESULT 6  
US-10-473-207-25  
; Sequence 25, Application US/10473207  
; Publication No. US20040163145A1  
; GENERAL INFORMATION:  
; APPLICANT: Maliga, Pal  
; APPLICANT: Cornelle, Sylvie  
; APPLICANT: Lutz, Kerry  
; TITLE OF INVENTION: Integrases for the insertion of heterologous nucleic acids into the plastid genome  
; FILE REFERENCE: 1594-RUT-01-091US  
; CURRENT APPLICATION NUMBER: US/10/473,207  
; CURRENT FILING DATE: 2003-03-19  
; PRIORITY APPLICATION NUMBER: PCT/US02/09537  
; PRIORITY FILING DATE: 2002-03-29  
; PRIORITY APPLICATION NUMBER: 60/279615  
; NUMBER OF SEQ ID NOS: 29  
; SEQ ID NO 25  
; LENGTH: 2391  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: plasmid fragment  
; US-10-473-207-25

Query Match 89.8%; Score 119.4; DB 7; Length 2391;  
Best Local Similarity 98.5%; Pred. No. 3.1e-34; Mismatches 1; Indels 1; Gaps 1;  
Matches 131; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCCGCGTCGTCAATGAGAATGATGAGGCTCGTGGATGACGTTGAGGGGG 60  
Db 13 GCTCCCCCGCCGCGTCGTCAATGAGAATGATGAGGCTCGTGGATGACGTTGAGGGGG 72

QY 61 CAGGGATGCATA-TTCGGGAGGAACTCCGGGCAATACGAGCCTTGAAATACAGT 119

RESULT 7  
US-10-881-813-6  
; Sequence 6, Application US/10881813  
; Publication No. US20050044593A1  
; GENERAL INFORMATION:  
; APPLICANT: Cox, Kevin  
; APPLICANT: Peele, Charles G.  
; TITLE OF INVENTION: Chloroplast Transformation of Duckweed  
; FILE REFERENCE: 40589/27994  
; CURRENT APPLICATION NUMBER: US/10/881,813  
; CURRENT FILING DATE: 2004-06-30  
; PRIORITY APPLICATION NUMBER: US 60/484,166  
; PRIORITY FILING DATE: 2003-07-01  
; PRIORITY APPLICATION NUMBER: US 60/492,179  
; NUMBER OF SEQ ID NOS: 12  
; SEQ ID NO 6  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; PRIORITY APPLICATION NUMBER: US 60/484,166  
; PRIORITY FILING DATE: 2003-07-01  
; PRIORITY APPLICATION NUMBER: US 60/492,179  
; NUMBER OF SEQ ID NOS: 12  
; SEQ ID NO 6  
; LENGTH: 119  
; TYPE: DNA  
; ORGANISM: Nicotiana tabacum  
; US-10-881-813-6

Query Match 80.5%; Score 107; DB 8; Length 119;  
Best Local Similarity 99.2%; Pred. No. 7.7e-30; Mismatches 0; Indels 1; Gaps 1;  
Matches 118; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCCGCGTCGTCAATGAGAATGATGAGGCTCGTGGATGACGTTGAGGGGG 60  
Db 61 CAGGGATGCATA-TTCGGGAGGAACTCCGGGCAATACGAGCCTTGAAATACAG 118  
QY 61 CAGGGATGCATA-TTCGGGAGGAACTCCGGGCAATACGAGCCTTGAAATACAG 119

RESULT 8  
US-10-095-514-3  
; Sequence 3, Application US/10095514  
; Publication No. US20040093636A1  
; GENERAL INFORMATION:  
; APPLICANT: Saeki, Yukiko  
; APPLICANT: Yokota, Akiho  
; APPLICANT: Madoka, Yuka  
; TITLE OF INVENTION: Method for Promoting Fatty Acid Synthesis in a Plant  
; FILE REFERENCE: 026350-072  
; CURRENT APPLICATION NUMBER: US/10/095,514  
; CURRENT FILING DATE: 2002-03-13  
; PRIORITY APPLICATION NUMBER: JP 2001-70,691  
; PRIORITY FILING DATE: 2001-03-13  
; PRIORITY APPLICATION NUMBER: JP 2001-300,038  
; PRIORITY FILING DATE: 2001-09-28  
; NUMBER OF SEQ ID NOS: 11  
; SEQ ID NO 3  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 220  
; TYPE: DNA  
; ORGANISM: N. tabacum cv. Xanthi  
; US-10-095-514-3

Query Match 77.3%; Score 102.9; DB 7; Length 220;  
Best Local Similarity 90.3%; Pred. No. 3.3e-28; Mismatches 12; Indels 1; Gaps 1;  
Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCCGCGTCGTCAATGAGAATGATGAGGCTCGTGGATGACGTTGAGGGGG 60

RESULT 9  
US-10-737-251-3B  
Sequence 38, Application US/10737251  
Publication No. US20040221338A1  
; GENERAL INFORMATION:  
; APPLICANT: Pal Maliga  
; TITLE OF INVENTION: Plastid rRNA Operon PromoterElements for Transgene Expression  
; FILE REFERENCE: 1594 RUT 03-083US  
; CURRENT APPLICATION NUMBER: US/10/737, 251  
; CURRENT FILING DATE: 2003-12-15  
; PRIORITY APPLICATION NUMBER: 60/433, 302  
; PRIORITY FILING DATE: 2002-12-13  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 38  
; LENGTH: 233  
; TYPE: DNA  
; ORGANISM: Nicotiana tabacum  
; US-10-737-251-3B

Query Match Best Local Similarity 77.3%; Score 102.8; DB 8; length 233; Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 1 GTCGCCCGCGCTCGTCAATGAGAATGGATGAGCTGGGAGGGGG 60  
Db 34 GTCGCCCGCGCTCGTCAATGAGAATGGATGAGCTGGGAGGGGG 93

Qy 61 CAGGGATGGCTATA-TCTGGGGGGAACCTCGGGGGAATACGAAAGGGCTGGATAGCT 119  
Db 94 CAGGGATGGCTATA-TCTGGGGGGAACCTCGGGGGAATACGAAAGGGCTGGATAGCT 153

Qy 120 TGTAGGGAGGATT 133  
Db 154 TTATGCCTTGGAAT 167

RESULT 10  
US-10-377-134-63/c  
Sequence 63, Application US/10377134  
; Publication No. US20040096938A1  
; GENERAL INFORMATION:  
; APPLICANT: XU, Ming-Qun  
; APPLICANT: EVANS, Thomas C.  
; APPLICANT: PRADHAN, Sriharsha  
; APPLICANT: COMB, Donald G.  
; APPLICANT: PAULUS, Henry  
; APPLICANT: SUN, Luo  
; APPLICANT: CHEN, Lixin  
; APPLICANT: GHOSH, Ima  
; TITLE OF INVENTION: METHOD FOR GENERATING SPLIT, NON-TRANSFERABLE GENES  
; FILE REFERENCE: NBR-219  
; CURRENT APPLICATION NUMBER: US/10/377, 134  
; CURRENT FILING DATE: 2003-02-28  
; PRIORITY APPLICATION NUMBER: 09/935, 588  
; PRIORITY FILING DATE: 2002-03-29  
; PRIORITY APPLICATION NUMBER: PCT/US00/14122  
; PRIORITY FILING DATE: 2000-05-23  
; PRIORITY APPLICATION NUMBER: 60/135, 677

Query Match Best Local Similarity 77.3%; Score 102.8; DB 7; length 7652; Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 1 GTCGCCCGCGCTCGTCAATGAGAATGGATAGAGGCTCTGGGATGAGCTGGGGGG 60  
Db 6644 GTCGCCCGCGCTCGTCAATGAGAATGGATAGAGGCTCTGGGATGAGCTGGGGGG 6585

Qy 61 CAGGGATGGCTATA-TCTGGGGGGAACCTCGGGGGAATACGAAAGGGCTGGGATGAGCTGGGGGG 119  
Db 6584 CAGGGATGGCTATA-TCTGGGGGGAACCTCGGGGGAATACGAAAGGGCTGGGATGAGCTGGGGGG 6525

Qy 120 TGTAGGGAGGATT 133

RESULT 11  
US-10-680-824A-1/c  
Sequence 1, Application US/10680824A  
; Publication No. US20040133937A1  
; GENERAL INFORMATION:  
; APPLICANT: Boudreau, Eric  
; APPLICANT: Gu, Weinig  
; APPLICANT: De Framond, Anne  
; APPLICANT: Heifetz, Peter  
; TITLE OF INVENTION: Plastid Transformation  
; FILE REFERENCE: 70149USNP  
; CURRENT APPLICATION NUMBER: US/10/680, 824A  
; CURRENT FILING DATE: 2003-10-07  
; PRIORITY APPLICATION NUMBER: 60/418596  
; PRIORITY FILING DATE: 2002-07-10  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 1  
; LENGTH: 7652  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; OTHER INFORMATION: pBPPOT plastid transformation vector (Example 1 VII).  
; US-10-680-824A-1

Query Match Best Local Similarity 77.3%; Score 102.8; DB 7; length 7652; Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 1 GTCGCCCGCGCTCGTCAATGAGAATGGATAGAGGCTCTGGGATGAGCTGGGGGG 60  
Db 6644 GTCGCCCGCGCTCGTCAATGAGAATGGATAGAGGCTCTGGGATGAGCTGGGGGG 6585

Qy 61 CAGGGATGGCTATA-TCTGGGGGGAACCTCGGGGGAATACGAAAGGGCTGGGATGAGCTGGGGGG 119  
Db 6584 CAGGGATGGCTATA-TCTGGGGGGAACCTCGGGGGAATACGAAAGGGCTGGGATGAGCTGGGGGG 6525

Db 6524 TTATGCCCTTGTGAAT 6511

RESULT 12

; Sequence 2, Application US/10680824A

; GENERAL INFORMATION:

; APPLICANT: Boudreau, Eric

; APPLICANT: Gu, Weinig

; APPLICANT: De Framond, Anic

; APPLICANT: Heifetz, Peter

TITLE OF INVENTION: Plasmid Transformation

FILE REFERENCE: 70149USNP

CURRENT APPLICATION NUMBER: US/10/680, 824A

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/418596

PRIOR FILING DATE: 2002-07-10

SEQ ID NO 2

LENGTH: 8684

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: PEBB (= PBBBa) plastid transformation vector (Example 2).

US-10-680-824A-2

Query Match 77.3%; Score 102.8; DB 7; Length 8684;

Best Local Similarity 90.3%; Pred. No. 7.1e-28; Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 GCTCCCCCCCCTGGTGTTCATGAGATAAGGGCTGTGGATTGACGTGAGGGG 60

Db 2492 GCTCCCCCGCCGGTGTCAATGAGATGGTAAAGGGCTCGGGATTGACGTGAGGGG 2551

QY 61 CAGGGATGGCTATA-TTCUGGGAGGAACTCCGGGATACAGAGCCTTGATACAGT 119

Db 2552 CAGGGATGGCTATA-TTCUGGGAGGAACTCCGGGCAATATGAGCCTGGATACAG 2611

Qy 120 TGTAGGGAGGGATT 133

Db 2612 TTATGCCCTTGTGAAT 2625

RESULT 13

US-10-680-824A-19

; Sequence 19, Application US/10680824A

; Publication No. US20040133937A1

; GENERAL INFORMATION:

; APPLICANT: Boudreau, Eric

; APPLICANT: Gu, Weinig

; APPLICANT: De Framond, Anic

; APPLICANT: Heifetz, Peter

TITLE OF INVENTION: Plastid Transformation

FILE REFERENCE: 70149USNP

CURRENT APPLICATION NUMBER: US/10/680, 824A

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/418596

PRIOR FILING DATE: 2002-07-10

SEQ ID NO 19

LENGTH: 10011

TYPE: DNA

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: plasmid

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)..(10011)

US-10-957-562-4

Query Match 77.3%; Score 102.8; DB 9; Length 10011;

Best Local Similarity 90.3%; Pred. No. 7.3e-28; Matches 121; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 1 GCTCCCCCCCCTGGTGTTCATGAGATAAGGGCTGTGGATTGACGTGAGGGG 60

Db 4372 GCTCCCCCGCCGGTGTCAATGAGATGGTAAAGGGCTCGGGATTGACGTGAGGGG 4431

Qy 61 CAGGGATGGCTATA-TTCUGGGAGGAACTCCGGGATACAGAGCCTTGATACAGT 119

Db 4432 CAGGGATGGCTATA-TTCUGGGAGGAACTCCGGGCAATATGAGCCTGGATACAG 4491

Qy 120 TGTAGGGAGGGATT 133

Db 4492 TTATGCCCTTGTGAAT 4505

RESULT 15

US-10-680-824A-2/C

; Sequence 2, Application US/10680824A

; Publication No. US20040133937A1

; GENERAL INFORMATION:

; APPLICANT: Boudreau, Eric

; APPLICANT: Gu, Weinig

; APPLICANT: De Framond, Anic

; APPLICANT: Heifetz, Peter

TITLE OF INVENTION: Plastid Transformation

FILE REFERENCE: 70149USNP

CURRENT APPLICATION NUMBER: US/10/680, 824A

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/418596

PRIOR FILING DATE: 2002-07-10

NUMBER OF SEQ ID NOS: 29

SEQ ID NO 19

LENGTH: 10011

TYPE: DNA

ORGANISM: artificial sequence

FEATURE:

OTHER INFORMATION: plasmid pEB10

US-10-680-824A-19

Query Match 77.3%; Score 102.8; DB 7; Length 10011;

BEST LOCAL SIMILARITY 90.3%; PRED. NO. 7.3e-28;

MATCHES 121; CONSERVATIVE 0; MISMATCHES 12; INDELS 1; GAPS 1;

NUMBER OF SEQ ID NOS: 29

QY 1 GCTCCCCCCCCTGGTGTTCATGAGATAAGGGCTGTGGATTGACGTGAGGGG 60

Db 4372 GCTCCCCCGCCGGTGTCAATGAGATAAGGGCTGTGGATTGACGTGAGGGG 4431

QY 61 CAGGGATGGCTATA-TTCUGGGAGGAACTCCGGGATACAGAGCCTTGATACAGT 119

Db 4432 CAGGGATGGCTATA-TTCUGGGAGGAACTCCGGGCAATATGAGCCTGGATACAG 4491

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 8684  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
;  
; OTHER INFORMATION: pEBB (= pEB8a) plastid transformation vector (Example 2).  
US-10-680-824A-2

Query Match 72.3%; Score 96.2; DB 7; Length 8684;  
Best Local Similarity 95.3%; P-reqd. No. 2.1e-25;  
Matches 121; Conservative 0; Mismatches 3; Indels 3; Gaps 2;  
Qy 8 CGCGGTCTTCAATGAGATGGATAAGGGCTGGATGACGTGAGGGCCAGGGAT 67  
Db 506 CGCGGTCTTCAATGAGATGGATAAGGGCTGGATGACGTGAGGGCCAGGGAT 447  
Qy 68 GGCTATA-TTCTGGAGCGAACCTCGGGCGAAATACGAGGCGCTGGATACGTGTAGGG 126  
Db 446 GGCTATA-TTCTGGAGCGAACCTCGGGCGAAATCTGAGGCCCTGGAT--AGTTGTRGGG 389  
Qy 127 AGGGATT 133  
Db 388 AGGGATT 382

Search completed: April 17, 2006, 23:57:07  
Job time : 455 secs

GenCore version 5.1.7  
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On nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:46:06 ; Search time 148 Seconds  
(without alignments)

1597.403 Million cell updates/sec

Title: US-10-663-241-32  
Perfect score: 133  
Sequence: 1 gctcccccggcgctgtccaa.....tacagttgttagggaggatt 133

Scoring table: IDENTITY\_NUC

Gpop 10.0 , Gapext 1.0

Searched: 1303057 seqs., 888780828 residues

Total number of hits satisfying chosen parameters:

2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgcn2\_6/ptodata/lina/1ina/1\_COMB.seq: \*  
2: /cgcn2\_6/ptodata/lina/5\_COMB.seq: \*  
3: /cgcn2\_6/ptodata/lina/6A\_COMB.seq: \*  
4: /cgcn2\_6/ptodata/lina/6B\_COMB.seq: \*  
5: /cgcn2\_6/ptodata/lina/H\_COMB.seq: \*  
6: /cgcn2\_6/ptodata/lina/PCTUS\_COMB.seq: \*  
7: /cgcn2\_6/ptodata/lina/PP\_COMB.seq: \*  
8: /cgcn2\_6/ptodata/lina/RE\_COMB.seq: \*  
9: /cgcn2\_6/ptodata/lina/backfiles.seq: \*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	133	100.0	133	US-09-445-283C-32
2	122	91.7	165	Sequence 32, Appl
3	122	91.7	165	Sequence 4, Appl
4	122	91.7	168	Sequence 2, Appl
5	122	91.7	168	Sequence 2, Appl
6	122	91.7	1134	Sequence 10, Appl
7	122	91.7	1143	Sequence 6, Appl
8	122	91.7	1416	Sequence 27, Appl
9	122	91.7	1415	Sequence 27, Appl
10	122	91.7	1417	Sequence 1, Appl
11	122	91.7	161	Sequence 18, Appl
12	121	91.0	161	Sequence 18, Appl
13	121	91.0	159	Sequence 18, Appl
14	121	91.0	300	Sequence 4, Appl
15	121	91.0	300	Sequence 7, Appl
16	121	91.0	1208	Sequence 28, Appl
17	121	91.0	1208	Sequence 1, Appl
18	118.8	89.3	150	Sequence 1, Appl
19	118.8	89.3	150	Sequence 1, Appl
20	102.8	77.3	184	Sequence 3, Appl
21	102.8	77.3	201	Sequence 58, Appl
C	102.8	77.3	2962	Sequence 3, Appl
C	102.8	77.3	2962	Sequence 3, Appl
C	102.8	77.3	6477	Sequence 63, Appl

#### ALIGNMENTS

RESULT 1  
US-09-445-283C-32  
; Sequence 32, Application US/09445283C  
; Patent No. 6624396  
; GENERAL INFORMATION:  
; APPLICANT: Maliga, Pal  
; APPLICANT: Sihavy, Daniel  
; APPLICANT: Sriramam, Priya  
; TITLE OF INVENTION: Plastid Promoters for Transgene Expression in the Plasmids of Higher Plants  
; FILE REFERENCE: Rut 97-0097  
; CURRENT APPLICATION NUMBER: US/09/445, 283C  
; CURRENT FILING DATE: 1999-12-03  
; PRIORITY APPLICATION NUMBER: PCT/US98/11437  
; PRIORITY FILING DATE: 1998-06-03  
; PRIORITY APPLICATION NUMBER: 60/048, 376  
; PRIORITY FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO: 32  
; LENGTH: 133  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Prrn promoter  
US-09-445-283C-32  
Query Match 100.0%; Score 133; DB 3; Length 133;  
Best Local Similarity 100.0%; Pred. No. 4.5e-39;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCCCCCGCCGTTGTCAATGAGAAATGATAGAGGCTCGTGGATTGACCGTGGAGCGG 60  
Db 1 GCTCCCCCGCCGTTGTCAATGAGAAATGAGCTCGTGGATTGACCGTGGAGCGG 60  
QY 61 CAGGGATGCTATTCCTGGAGGAGACTCCGGAGATAGAGCTTGATACGTT 120  
Db 61 CAGGGATGCTATTCCTGGAGGAGACTCCGGAGATAGAGCTTGATACGTT 120

RESULT 2

US-08-189-256A-4 ; Sequence 4, Application US/08189256A  
; Sequence No. 587402 ; Patent No. 6388168  
; GENERAL INFORMATION :  
; APPLICANT: Maliga, Pal ; GENERAL INFORMATION:  
; APPLICANT: Svab, Zora ; APPLICANT: Maliga, Pal  
; APPLICANT: Svab, Zora ; APPLICANT: Zoubenko, Oleg V.  
; APPLICANT: Zoubenko, Oleg V. ; APPLICANT: Svab, Zora  
; APPLICANT: Allison, Lori A. ; APPLICANT: Carrer, Helaine  
; APPLICANT: Carrer, Helaine ; APPLICANT: Kavevski, Ivan  
; APPLICANT: Kavevski, Ivan ; TITLE OF INVENTION: DNA Constructs and Methods for Stably  
; TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and  
; TITLE OF INVENTION: Expressing Recombinant Proteins Therein ; TITLE OF INVENTION: DNA Constructs and Methods for Stably  
; NUMBER OF SEQUENCES: 47 ; NUMBER OF SEQUENCES: 47 ; TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and  
; CORRESPONDENCE ADDRESS: ; CORRESPONDENCE ADDRESS: ; TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman ; ADDRESSEE: Dann, Dorfman, Herrell and Skillman  
; STREET: 1601 Market Street Suite 720 ; STREET: 1601 Market Street Suite 720  
; CITY: Philadelphia ; CITY: Philadelphia  
; STATE: PA ; STATE: PA  
; COUNTRY: USA ; COUNTRY: USA  
; ZIP: 19103-2307 ; ZIP: 19103-2307  
; COMPUTER READABLE FORM: ; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk ; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible ; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS ; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: ; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/189,256A ; APPLICATION NUMBER: US/08/189,256A  
; FILING DATE: 31-JAN-1994 ; FILING DATE: 31-JAN-1994  
; CLASSIFICATION: 435 ; CLASSIFICATION:  
; PRIOR APPLICATION DATA: ; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/111,398 ; APPLICATION NUMBER: US 08/111,398  
; FILING DATE: 25-AUG-1993 ; FILING DATE:  
; PRIOR APPLICATION DATA: ; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/518,763 ; APPLICATION NUMBER: US 07/518,763  
; FILING DATE: 01-MAY-1990 ; FILING DATE:  
; ATTORNEY/AGENT INFORMATION: ; ATTORNEY/AGENT INFORMATION:  
; NAME: Reed, Jane E. ; NAME: Reed, Jane E.  
; REGISTRATION NUMBER: 36,252 ; REGISTRATION NUMBER: 36,252  
; TELECOMMUNICATION INFORMATION: ; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 563-4100 ; TELEPHONE: (215) 563-4100  
; TELEFAX: (215) 563-4044 ; TELEFAX: (215) 563-4044  
; INFORMATION FOR SEQ ID NO: 4: ; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS: ; SEQUENCE CHARACTERISTICS:  
; LENGTH: 165 base pairs ; LENGTH: 165 base pairs  
; TYPE: nucleic acid ; TYPE: nucleic acid  
; STRANDEDNESS: single ; STRANDEDNESS: single  
; TOPOLOGY: linear ; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic) ; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO ; HYPOTHETICAL: NO  
; ANTI-SENSE: NO ; ANTI-SENSE: NO  
; US-08-189-256A-4 ; US-08-189-256A-4  
; Query Match 91.7%; Score 122; DB 2; Length 165;  
; Best Local Similarity 99.3%; Pred. No. 5.2e-35; Indels 1; Gaps 1;  
; Matches 133; Conservative 0; Mismatches 0;  
; Query 1 GCCTCCCCCGCCGCGTGTCAATGAGAAATGGATAAGAGCTCTGGGATGACGGCTGGGG 60  
; Db 1 GCTCCCCCGCCGCGTGTCAATGAGAAATGGATAAGAGCTCTGGGATGACGGCTGGGG 60  
; Query 61 CAGGGATGGCTATA-TTCGGGAGGCAACTCGGGGGAATACGACGCCCTGGATCAGT 119  
; Db 61 CAGGGATGGCTATA-TTCGGGAGGCAACTCGGGGGAATACGACGCCCTGGATCAGT 120  
; Query 120 TGTAGGGAGGATT 133  
; Db 121 TGTAGGGAGGATT 134  
; RESULT 3 ; RESULT 4  
; US-09-193-853-4 ; US-08-189-256A-2  
; ; Sequence 2, Application US/08189256A

Patent No. 5877402  
GENERAL INFORMATION:

APPLICANT: Maliga, Pal

APPLICANT: Strab, Zora

APPLICANT: Staub, Jeffrey

APPLICANT: Zoubenko, Oleg V.

APPLICANT: Allison, Lori A.

APPLICANT: Carrer, Helaine

APPLICANT: Kanevski, Ivan

TITLE OF INVENTION: DNA Constructs and Methods for Stably

TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and

TITLE OF INVENTION: Expressing Recombinant Proteins Therein

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman

STREET: 1601 Market Street Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/189,256A

FILING DATE: 31-JAN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/111,398

FILING DATE: 25-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/189,256A

FILING DATE: 31-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 563-4100

TELEFAX: (215) 563-4044

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 168 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPLOGY: not relevant

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-189-256A-2

Query Match 91.7%; Score 122; DB 2; Length 168;  
Best Local Similarity 99.3%; Pred. No. 5.2e-35; Mismatches 0; Indels 1; Gaps 1;

Matches 133; Conservative 0; MisMatches 0; Del 0; Insert 1; Gap 1;

Qy 1 GCTCCCCCGGCTGGTCAATGAGATGATGATAAGGGCTGGATGACGGCTGGAGGG 60  
Db 1 GCTCCCCCGGCTGGTCAATGAGATGATGATAAGGGCTGGATGACGGCTGGAGGG 60  
Qy 61 CAGGGATGCCTATA-TTCCTGGAGCGACTCCCGGGAATCAGGACCTGGCTGGATACAGT 119  
Db 61 CAGGGATGCCTATA-TTCCTGGAGCGACTCCCGGGAATCAGGACCTGGCTGGATACAGT 120  
Qy 120 TGTAGGGAGGATT 133  
Db 121 TGTAGGGAGGATT 134

RESULT 5

US-09-193-853-2

; Sequence 2, Application US/09193853

; Patent No. 6389168

GENERAL INFORMATION:  
APPLICANT: Maliga, Pal

APPLICANT: Svab, Zora

APPLICANT: Staub, Jeffrey

APPLICANT: Zoubenko, Oleg V.

APPLICANT: Allison, Lori A.

APPLICANT: Carrer, Helaine

APPLICANT: Kanevski, Ivan

TITLE OF INVENTION: DNA Constructs and Methods for Stably

TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and

TITLE OF INVENTION: Expressing Recombinant Proteins Therein

NUMBER OF SEQUENCES: 47

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dann, Dorfman, Herrell and Skillman

STREET: 1601 Market Street Suite 720

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/193,853

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/189,256

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/111,398

FILING DATE: 31-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 563-4100

TELEFAX: (215) 563-4044

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 168 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPLOGY: not relevant

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-193-853-2

Query Match 91.7%; Score 122; DB 3; Length 168;  
Best Local Similarity 99.3%; Pred. No. 5.2e-35; Mismatches 0; Indels 1; Gaps 1;

Matches 133; Conservative 0; MisMatches 0; Del 0; Insert 1; Gap 1;

Qy 1 GCTCCCCCGGCTGGTCAATGAGATGATGATAAGGGCTGGATGACGGCTGGAGGG 60  
Db 1 GCTCCCCCGGCTGGTCAATGAGATGATGATAAGGGCTGGATGACGGCTGGAGGG 60  
Qy 61 CAGGGATGCCTATA-TTCCTGGAGCGACTCCCGGGAATCAGGACCTGGCTGGATACAGT 119  
Db 61 CAGGGATGCCTATA-TTCCTGGAGCGACTCCCGGGAATCAGGACCTGGCTGGATACAGT 120  
Qy 120 TGTAGGGAGGATT 133  
Db 121 TGTAGGGAGGATT 134

RESULT 6

US-08-189-256A-10/c

; Sequence 2, Application US/08189256A

; Patent No. 5877402

; GENERAL INFORMATION:

APPLICANT: Maliga, Pal  
 APPLICANT: Svab, Zora  
 APPLICANT: Staub, Jeffrey  
 APPLICANT: Zoubenko, Oleg V.  
 APPLICANT: Alison, Lori A.  
 APPLICANT: Carrier, Helaine  
 APPLICANT: Kanevski, Ivan  
 TITLE OF INVENTION: DNA Constructs and Methods for Stably Transforming Plastids of Multicellular Plants and Expressing Recombinant Proteins Therein  
 TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
 NUMBER OF SEQUENCES: 47  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dunn, Dorfman, Hurrell and Skillman  
 STREET: 1601 Market Street Suite 720  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103-2307  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/189,256A  
 FILING DATE: 31-JAN-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/1518,763  
 FILING DATE: 01-MAY-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Reed, Janet E.  
 REGISTRATION NUMBER: 36,252  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 563-4100  
 TELEFAX: (215) 563-4044  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1134 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULAR TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-189-256A-10  
 Query Match 91.7%; Score 122; DB 2; Length 1134;  
 Best Local Similarity 99.3%; Pred. No. 1e-34; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 GCTTCCCCCGCCGCGTCATGAGATGAGCTGGGATGACCTGGGAGGGGG 60  
 Db 1058 GCTTCCCCCGCCGCGTCATGAGATGAGCTGGGATGACCTGGGAGGGGG 60  
 QY 61 CAGGGATGGCTATA-TTCTGGGAGGGAATCCTGGGCGATAGAAGGGCTTGATACGT 119  
 Db 998 CAGGGATGGCTATA-TTCTGGGAGGGAATCCTGGGCGATAGAAGGGCTTGATACGT 939  
 QY 120 TCTAGGAGGGATT 133  
 Db 938 TGTAGGAGGGATT 925  
 RESULT 7  
 US-09-193-853-10/C  
 Sequence 10, Application US/09193853  
 ; Patent No. 6388168  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Maliga, Pal

---

APPLICANT: Svab, Zora  
 APPLICANT: Staub, Jeffrey  
 APPLICANT: Zoubenko, Oleg V.  
 APPLICANT: Alison, Lori A.  
 APPLICANT: Carrier, Helaine  
 APPLICANT: Kanevski, Ivan  
 TITLE OF INVENTION: DNA Constructs and Methods for Stably Transforming Plastids of Multicellular Plants and Expressing Recombinant Proteins Therein  
 TITLE OF INVENTION: Expressing Recombinant Proteins Therein  
 NUMBER OF SEQUENCES: 47  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dunn, Dorfman, Hurrell and Skillman  
 STREET: 1601 Market Street Suite 720  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103-2307  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/193,853  
 FILING DATE: 01-MAY-1990  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/189,256  
 FILING DATE: 01-MAY-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Reed, Janet E.  
 REGISTRATION NUMBER: 36,252  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 563-4100  
 TELEFAX: (215) 563-4044  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1134 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULAR TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-09-193-853-10  
 Query Match 91.7%; Score 122; DB 3; Length 1134;  
 Best Local Similarity 99.3%; Pred. No. 1e-34; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 GCTTCCCCCGCCGCGTCATGAGATGAGCTGGGATGACCTGGGAGGGGG 60  
 Db 1058 GCTTCCCCCGCCGCGTCATGAGATGAGCTGGGATGACCTGGGAGGGGG 60  
 QY 61 CAGGGATGGCTATA-TTCTGGGAGGGAATCCTGGGCGATAGAAGGGCTTGATACGT 119  
 Db 998 CAGGGATGGCTATA-TTCTGGGAGGGAATCCTGGGCGATAGAAGGGCTTGATACGT 939  
 QY 120 TCTAGGAGGGATT 133  
 Db 938 TGTAGGAGGGATT 925  
 RESULT 8  
 US-09-142-114B-6/C  
 Sequence 6, Application US/09142114B  
 ; Patent No. 6376744  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rutgers University  
 ; APPLICANT: Maliga, Pal

APPLICANT: Reddy, Siva Vanga  
 APPLICANT: Sikdar, Samir R.  
 TITLE OF INVENTION: Plastid Transformation in Arabidopsis  
 TITLE OF INVENTION: Thaliana  
 FILE REFERENCE: 09/142,114  
 CURRENT APPLICATION NUMBER: US/09/142,114B  
 CURRENT FILING DATE: 1999-02-05  
 PRIORITY APPLICATION NUMBER: PCT/US97/0344  
 PRIORITY FILING DATE: 1997-03-06  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: FastSEQ for Windows Version 3.0  
 SEQ ID NO: 6  
 LENGTH: 1143  
 TYPE: DNA  
 ORGANISM: Nicotiana tabacum  
 ; US-09-142-114B-6  
 ;  
 Query Match 91.7%; Score 122; DB 3; Length 1143;  
 Best Local Similarity 99.3%; Pred. No. 1e-34; Mismatches 0; Indels 1; Gaps 1;  
 Matches 133; Conservative 0; MisMatches 0; Indels 1; Gaps 1;  
 ;  
 GENERAL INFORMATION:  
 Patient No. 5877402  
 ;  
 APPLICANT: Maliga, Pal  
 APPLICANT: Svab, Zora  
 APPLICANT: Staub, Jeffrey  
 APPLICANT: Zoubenko, Oleg V.  
 APPLICANT: Allison, Lori A.  
 APPLICANT: Carrer, Helaine  
 APPLICANT: Kaeverski, Ivan  
 ;  
 NUMBER OF SEQUENCES: 47  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dann, Dorfman, Harrell and Skillman  
 STREET: 1601 Market Street Suite 720  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103-2307  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ;  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/189,256A  
 FILING DATE: 25-AUG-1993  
 CLASSIFICATION: 431-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/111,398  
 FILING DATE: 01-MAY-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Reed, Janet E.  
 NAME: Reed, Janet E.  
 REGISTRATION NUMBER: 36,252  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 563-4100  
 TELEFAX: (215) 563-4044  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1416 base pairs  
 TYPE: nucleic acid  
 STRANDBNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ; US-08-189-256A-27  
 ;  
 Query Match 91.7%; Score 122; DB 2; Length 1416;  
 Best Local Similarity 99.3%; Pred. No. 1.e-34; Mismatches 0; Indels 1; Gaps 1;  
 Matches 133; Conservative 0; MisMatches 0; Indels 1; Gaps 1;  
 ;  
 GENERAL INFORMATION:  
 Patient No. 638868  
 ;  
 APPLICANT: Maliga, Pal  
 APPLICANT: Svab, Zora  
 APPLICANT: Staub, Jeffrey  
 APPLICANT: Zoubenko, Oleg V.  
 APPLICANT: Allison, Lori A.  
 APPLICANT: Carrer, Helaine  
 APPLICANT: Kaeverski, Ivan  
 ;  
 NUMBER OF SEQUENCES: 47  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dann, Dorfman, Harrell and Skillman  
 STREET: 1601 Market Street Suite 720  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103-2307  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ;  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/193,853  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/189,256  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/518,763  
 FILING DATE: 01-MAY-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Reed, Janet E.

REGISTRATION NUMBER: 36,252  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 563-4100  
 TELFAX: (215) 563-4044  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1416 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-09-193-853-27

Query Match 91.7%; Score 122; DB 3; Length 1417;  
 Best Local Similarity 99.3%; Pred. No. 1.1e-34; Mismatches 0; Indels 1; Gaps 1;  
 Matches 133; Conservative 0; ;  
 Qy 1 GCTCCCCCGCCGCTGGTCAATGAGAATGGATAAGACCTCTGGATGACGTGAGGGG 60  
 Db 23 GCTCCCCCGCCGCTGGTCAATGAGAATGGATAAGACCTCTGGATGACGTGAGGGG 82  
 Qy 61 CAGGGATGCTATA-TTCGGAGGAACTCCGGCGATACTGAGGGCTTGATAGT 119  
 Db 83 CAGGGATGCTATA-TTCGGAGGAACTCCGGCGATACTGAGGGCTTGATAGT 142  
 Qy 120 TGTAGGGAGGGATT 132  
 Db 142 TGTAGGGAGGGATT 155

RESULT 11  
 US-09-142-114B-7  
 Sequence 7, Application US/09142114B  
 Patent No. 6376744

GENERAL INFORMATION:  
 APPLICANT: Rutgers University  
 ADDRESS: Piscataway, NJ 08854-2984  
 CITY: Piscataway  
 STATE: NJ  
 ZIP: 08854-2984  
 COUNTRY: USA  
 ZIP: 08854-2984  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/189,256A  
 FILING DATE: 31-JAN-1994  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/111,398  
 FILING DATE: 25-AUG-1993  
 FILING DATE: 01-MAY-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Reed, Janet E.  
 REGISTRATION NUMBER: 36,252  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 563-4100  
 TELFAX: (215) 563-4044  
 INFORMATION FOR SEQ ID NO: 18:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 161 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-09-142-114B-7

Query Match 91.0%; Score 121; DB 2; Length 161;  
 Best Local Similarity 99.2%; Pred. No. 1.2e-34; Mismatches 0; Indels 1; Gaps 1;  
 Matches 132; Conservative 0; ;  
 Qy 1 GCTCCCCCGCCGCTGGTCAATGAGAATGGATAAGACCTCTGGATGACGTGAGGGG 60  
 Db 23 GCTCCCCCGCCGCTGGTCAATGAGAATGGATAAGACCTCTGGATGACGTGAGGGG 82  
 Qy 61 CAGGGATGCTATA-TTCGGAGGAACTCCGGCGATACTGAGGGCTTGATAGT 119  
 Db 83 CAGGGATGCTATA-TTCGGAGGAACTCCGGCGATACTGAGGGCTTGATAGT 142  
 Qy 120 TGTAGGGAGGGATT 132  
 Db 143 TGTAGGGAGGGATT 155

RESULT 13

US-09-193-853-18

Sequence 18; Application US/09193853

Patent No. 6388168

GENERAL INFORMATION:

APPLICANT: Maliga, Pal

APPLICANT: Svab, Zora

APPLICANT: Staub, Jeffrey

APPLICANT: Zoubenko, Oleg V.

APPLICANT: Allison, Lori A.

APPLICANT: Carrer, Helaine

APPLICANT: Kanevski, Ivan

TITLE OF INVENTION: DNA Constructs and Methods for Stably Expressing Recombinant Proteins Therein

TITLE OF INVENTION: Transforming Plastids of Multicellular Plants and

TITLE OF INVENTION: Editing-Based Selectable Plastid Marker

TITLE OF INVENTION: Genes

FILE REFERENCE: Rat-96-06041

CURRENT APPLICATION NUMBER: US/09/202,316

CURRENT FILING DATE: 1999-06-01

PRIORITY NUMBER: PCT/US97/10318

PRIORITY FILING DATE: 1997-06-13

PRIORITY APPLICATION NUMBER: 60/019,741

PRIORITY FILING DATE: 1996-06-14

NUMBER OF SEQ ID NOS: 60

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 4

LENGTH: 300

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Synthetic Sequence

US-09-202-316-4

Query Match

Best Local Similarity 99.2%; Score 121; DB 3; Length 300;

Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

SEQ ID NO: 1

GCTCCCCCCCGRGTCTCATGAGAATGAGATAAGAGGCTCGTGGATTCACGTTGAGGG 60

Db

17 GCTCCCCCCCGRGTCTCATGAGAATGAGATAAGAGGCTCGTGGATTCACGTTGAGGG 76

SEQ ID NO: 61

CAGGGATGCTATA-TCTGGAGGGACTCCGGGAATACGAGGCCTGGTCAACGTT 119

Db

77 CAGGGATGCTATA-TCTGGAGGGACTCCGGGAATACGAGGCCTGGTCAACGTT 136

SEQ ID NO: 120 TGTAGGGAGGGAT 132

Db

137 TGTAGGGAGGGAT 149

RESULT 14

US-09-202-316-4

Sequence 4; Application US/09202316

PATENT NO. 6297054

GENERAL INFORMATION:

APPLICANT: Pal Maliga

APPLICANT: Helaine Carrer

APPLICANT: Sumita Chaudhuri

APPLICANT: Lori A. Allison

APPLICANT: Jeffrey Staub

APPLICANT: Oleg V. Zoubenko

APPLICANT: Ivan Kanevski

TITLE OF INVENTION: Genes

FILE REFERENCE: Rat-96-06041

CURRENT APPLICATION NUMBER: US/09/202,316

CURRENT FILING DATE: 1999-06-01

PRIORITY NUMBER: PCT/US97/10318

PRIORITY FILING DATE: 1997-06-13

PRIORITY APPLICATION NUMBER: 60/019,741

PRIORITY FILING DATE: 1996-06-14

NUMBER OF SEQ ID NOS: 60

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 7

LENGTH: 300

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: Other Information

OTHER INFORMATION: Synthetic Sequence

RESULT 15

US-09-202-316-7

Sequence 7; Application US/09202316

PATENT NO. 6297054

GENERAL INFORMATION:

APPLICANT: Pal Maliga

APPLICANT: Helaine Carrer

APPLICANT: Sumita Chaudhuri

APPLICANT: Lori A. Allison

APPLICANT: Jeffrey Staub

APPLICANT: Oleg V. Zoubenko

APPLICANT: Ivan Kanevski

TITLE OF INVENTION: Editing-Based Selectable Plastid Marker

TITLE OF INVENTION: Genes

FILE REFERENCE: Rat-96-06041

CURRENT APPLICATION NUMBER: US/09/202,316

PRIORITY APPLICATION NUMBER: PCT/US97/10318

PRIORITY FILING DATE: 1997-06-13

PRIORITY FILING DATE: 1996-06-14

NUMBER OF SEQ ID NOS: 60

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 7

LENGTH: 300

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: Other Information

OTHER INFORMATION: Synthetic Sequence

RESULT 16

US-09-202-316-7

Query Match

91.0%; Score 121; DB 3; Length 300;

Best Local Similarity 99.2%; Pred. No. 1.5e-34; Matches 132; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY	1	GCTGCCCGCCGCTGTCAATGAGATGGTAAAGGGCTGGATTGACCGTGAGGGGG	60
Db	17	GCTCCCCCGCCGCGTCATAAGAATGGTAAAGGGCTGGATTGACCGTGAGGGGG	76
QY	61	CAGGGATGGCTATA-TTCTGGAGCGGAATCCGGGGATACGAAGGCCTGGATACGT	119
Db	77	CAGGGATGGCTATA-TTCTGGAGCGGAATCCGGGGATACGAAGGCCTGGATACGT	136
QY	120	TCTAGGGAGGGAT	132
Db	137	TCTAGGGAGGGAT	149

Search completed: April 18, 2006, 00:25:54  
Job time : 149 secs



**RESULT 2**

Db 154 GCTGCCCGCCGCGTCAATGAGAATGGATAAGGGCTGGGAGTCGGGAACTCCGGGGAATCGAACGGCTTGATGAGT 95  
 LOCUS CN930271 DEFINITION 00322AFBC002396HT (AFBC) Royal Gala pre-opened floral bud Malus x domestica cDNA clone AFBC002396, mRNA sequence.

ACCESSION CN972595 VERSION CNB72595.1 GI:48258753  
 SOURCE EST  
 ORGANISM Malus x domestica

REFERENCE 61 CAGGGATGCATA-TTCGGAGGAGACTCCGGGGAATACGAGCCTTGATAGCT 119  
 AUTHORS Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., Walton,E. and Yauk,Y.  
 TITLE HortResearch Apple EST Project  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Gleave,A.  
 Sequencing Facility: The Horticulture and Food Research Institute of New Zealand Ltd  
 Tel: 00 64 09 815 4200  
 Fax: 00 64 09 815 4201  
 Email: est@hortresearch.co.nz.

**FEATURES source**

FEATURES location/Qualifiers

source 1. -415 /organism="Malus x domestica"  
 /mol\_type="mRNA"/db\_xref="AFBC002396"/>  
 /db\_xref="taxon:3750"/clone="AFBC002396"/tissue\_type="fruit"/>  
 /clone="AFBC002396"/dev\_stagex="24 days after full bloom"/>  
 /tissue\_type="Floral bud"/>  
 /tissue\_type="pre-opening, flower at stage of nectar/pollen formation"/>  
 /clone\_lib=" (AFBC) Royal Gala pre-opened floral bud"  
 /notes="Vector: PBK-CMV; library sequenced by Genesis Research & Development"

**ORIGIN**

Query Match 68.9%; Score 91.6; DB 7; Length 415;  
 Best Local Similarity 85.1%; Pred. No. 6.1e-19; Matches 114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

Db 196 GCTGCCCGCCGCGTCAATGAGAATGGATAAGGGCTGGGAGTCGGGAACTCCGGGGAATCGAACGGCTTGATGAGT 60  
 LOCUS CN930271 DEFINITION 00322AFBC002396HT (AFBC) Royal Gala pre-opened floral bud Malus x domestica cDNA clone AFBC002396, mRNA sequence.

ACCESSION AJB876197 VERSION AJB876197.1 GI:59932682  
 SOURCE EST  
 ORGANISM Prunus persica (peach)

REFERENCE 61 CAGGGATGCATA-TTCGGAGGAGACTCCGGGGAATACGAGCCTTGATAGCT 119  
 AUTHORS Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., Walton,E. and Yauk,Y.  
 TITLE HortResearch Apple EST Project  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Gleave,A.  
 Sequencing Facility: The Horticulture and Food Research Institute of New Zealand Ltd  
 Tel: 00 64 09 815 4200  
 Fax: 00 64 09 815 4201  
 Email: est@hortresearch.co.nz.

**FEATURES source**

FEATURES location/Qualifiers

source 1. -498 /organism="Malus x domestica"/mol\_type="mRNA"/>  
 /db\_xref="taxon:3750"/clone="AFPA005328"/>  
 /tissue\_type="fruit"/>  
 /dev\_stagex="24 days after full bloom"/>  
 /clone\_lib=" (AFPA) Royal Gala 24 DAFB fruit"/>  
 /note="Vector: PBK-CMV; library sequenced by Genesis Research & Development"

**ORIGIN**

Query Match 68.9%; Score 91.6; DB 7; Length 498;  
 Best Local Similarity 85.1%; Pred. No. 6.2e-19; Matches 114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

Db 307 TAGGATGCATA-TTCGGAGGAGACTCCGGGGAATCGAACGGCTTGATGAGT 306  
 LOCUS AJB876197 DEFINITION AJB876197 Prunus persica fruit mesocarp plus epidermis 80 days after bloom Prunus persica cDNA clone PR0213A05, mRNA sequence.

ACCESSION AJB876197 VERSION AJB876197.1 GI:59932682  
 SOURCE EST  
 ORGANISM Prunus persica (peach)

REFERENCE 61 CAGGGATGCATA-TTCGGAGGAGACTCCGGGGAATACGAGCCTTGATAGCT 119  
 AUTHORS Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., Walton,E. and Yauk,Y.  
 TITLE HortResearch Apple EST Project  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Gleave,A.  
 Sequencing Facility: The Horticulture and Food Research Institute of New Zealand Ltd  
 Tel: 00 64 09 815 4200  
 Fax: 00 64 09 815 4201  
 Email: est@hortresearch.co.nz.

**FEATURES source**

FEATURES location/Qualifiers

source 1. -380 /organism="Prunus persica (L.) Batsch" /mol\_type="mRNA"/>  
 /db\_xref="AFPA005328"/>  
 /clone="AFPA005328"/>  
 /tissue\_type="fruit"/>  
 /dev\_stagex="24 days after full bloom"/>  
 /clone\_lib=" (AFPA) Royal Gala 24 DAFB fruit"/>  
 /note="Vector: PBK-CMV; library sequenced by Genesis Research & Development"

**ORIGIN**

Query Match 68.9%; Score 91.6; DB 7; Length 415;  
 Best Local Similarity 85.1%; Pred. No. 6.1e-19; Matches 114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

Db 316 TTAGGCCTGGAAAT 380  
 LOCUS AJB876197 DEFINITION AJB876197 Prunus persica fruit mesocarp plus epidermis 80 days after bloom Prunus persica cDNA clone PR0213A05, mRNA sequence.

ACCESSION AJB876197 VERSION AJB876197.1 GI:59932682  
 SOURCE EST  
 ORGANISM Prunus persica (peach)

REFERENCE 61 CAGGGATGCATA-TTCGGAGGAGACTCCGGGGAATACGAGCCTTGATAGCT 119  
 AUTHORS Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., Walton,E. and Yauk,Y.  
 TITLE HortResearch Apple EST Project  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Gleave,A.  
 Sequencing Facility: The Horticulture and Food Research Institute of New Zealand Ltd  
 Tel: 00 64 09 815 4200  
 Fax: 00 64 09 815 4201  
 Email: est@hortresearch.co.nz.

**RESULT 3**

LOCUS CN872595 DEFINITION 020807AAPA005328HT (AAPA) Royal Gala 24 DAFB fruit Malus x domestica cDNA clone AAPA005328, mRNA sequence.

**source**

1. -510  
*/organism="Prunus persica"*  
*/mol\_type="mRNA"*  
*/cultivar="Fantasia"*  
*/db\_xref="taxon:3760"*  
*/clone="PR0213A05"*  
*/tissue\_type="fruit mesocarp plus epidermis"*  
*/dev\_stage="80 days after bloom"*  
*/clone\_lib="Prunus persica fruit mesocarp plus epidermis"*  
*80 days after bloom"*

**ORIGIN**

**Query Match** Best Local Similarity 68.9%; Score 91.6; DB 1; Length 510;  
 Matches 114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

**Qy** 1 GCTCCCGCGGCTGTCATGAGATGGATAAGGGCTGTGGGATGACGTGGGG 442

**Db** 383 GCTCCCGCGGCTGATGAGATGGATAAGGGCTGTGGGATGACGTGGGG 442

**Qy** 61 CAGGGTGCCTATA-TCTCGGAGGAACTTCGGCGGAAATACGAAGCGCTTGATCACT 119

**Db** 443 TAGGGATGGCTATATTCTCGGAGCAGTCAGGGATATGAGCATGAGCATGATAAG 502

**Qy** /dev\_stage="80 days after bloom"

**Db** 120 TGTAGGGAGGATT 133

**Qy** 503 TTATGCTTGGAT 516

**RESULT 5** CN871707 CN871707 598 bp mRNA linear EST 04-JUN-2004

**DEFINITION** 010128APA001324HT (APA) Royal Gala 24 DAFB fruit Malus x domestica cDNA clone APA001324, mRNA sequence.

**ACCESSION** CN871707

**VERSION** CN871707.1

**KEYWORDS** EST.

**SOURCE** Malus x domestica

**ORGANISM** Malus x domestica

**REFERENCE** 1 (bases 1 to 598)

**AUTHORS** Beuning, L., Bowen, J., Crowhurst, R., Gleave, A., Janssen, B., Martiney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.

**TITLE** HortResearch Apple EST Project

**JOURNAL** Unpublished (2004)

**COMMENT** Contact: Gleave,A.

**SEQUENCING FACILITY** The Horticulture and Food Research Institute of New Zealand Ltd

**120 Mt Albert Rd, Mt Albert, Auckland, New Zealand**

**TEL:** 00 64 09 815 4200

**FAX:** 00 64 09 815 4201

**EMAIL:** est@hortresearch.co.nz.

**FEATURES source**

1. .598  
*/organism="Malus x domestica"*  
*/mol\_type="mRNA"*  
*/db\_xref="taxon:3750"*  
*/clone="APA001324"*  
*/tissue\_type="fruit"*  
*/dev\_stage="24 days after full bloom"*  
*/clone\_lib="APA01324"*  
*/note="Vector: pk-CMV, Library sequenced by Genesis Research & Development"*

**ORIGIN**

**Query Match** Best Local Similarity 85.1%; Score 91.6; DB 7; Length 598;  
 Matches 114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;

**Qy** 1 GCTCCCCCGCGCTGTCATGAGATGGATAAGGGCTGTGGGATGACGTGGGG 60

**Db** 383 GCTCCCGCGGCTGATGAGATGGATAAGGGCTGTGGGATGACGTGGGG 442

**Qy** /dev\_stage="80 days after bloom"

**Db** 607 GACTTGAT 598

**RESULT 6** BH515735/c BH515735 763 bp DNA linear GSS 13-DEC-2001

**DEFINITION** BOHKC79R BOHK Brassica oleracea genomic clone BOHKC79, genomic survey sequence.

**ACCESSION** BH515735

**VERSION** BH515735.1 GI:17723825

**KEYWORDS** GSS.

**SOURCE** Brassica oleracea

**ORGANISM** Brassica oleracea

**REFERENCE** 1 (bases 1 to 763)

**AUTHORS** Ayle, N., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utterback, R.R., Wortman, J.R., White, O.R., and Town, C.D.

**TITLE** Whole genome shotgun sequencing of *Brassica oleracea* and its application to gene discovery and annotation in *Arabidopsis*

**JOURNAL** Genome Res. 15 (4), 487-495 (2005)

**PUBMED** 15805490

**COMMENT** Other\_GSS: BOHKC79TF

**CONTACT**: Chris Town

**TIGR** 9712 Medical Center Drive, Rockville, MD 20850, USA.

**TEL:** 301-838-3523

**FAX:** 301-838-0208

**EMAIL:** cdtown@tigr.org

DNA is from a double haploid provided by Tom Osborn.

**Seq primer:** TR Class: sheared endB.

**Location/Qualifiers**

1. .763  
*/organism="Brassica oleracea"*  
*/mol\_type="genomic DNA"*  
*/strain="TOI0000B3"*  
*/db\_xref="taxon:3712"*  
*/clone="BOHKC79"*  
*/clone.lib="BOHKC79"*  
*/note="Vector: phos1, Site1: BstXI; 2-3 kb sheared genomic DNA inserted into phos1 using BstXI linkers"*

**ORIGIN**

**Query Match** Best Local Similarity 81.5%; Score 91.6; DB 9; Length 763;  
 Matches 106; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

**Qy** 4 CCCCGGCCGCGTCAATGAGATGGATAAGGGCTGTGGGATGACGTGGGG 63

**Db** 727 CCCCGCGTGTGATGATGAGATGGATAAGGGCTGTGGGATGACGTGGGG 668

**Qy** 64 GGATGCGTATTCGGAGGAACTCCGGGGAATCCAGGCCTTGATCAGTTGA 123

**Db** 667 GGATGCGTATTCGGAGGAACTCCGGGGAATCCAGGCCTTGATCAGTTGA 608

**Qy** 124 GGGGGGAGATT 133

**Db** 607 GACTTGAT 598

**RESULT 7** CG026604/c CG026604 764 bp DNA linear GSS 19-AUG-2003

DEFINITION	PGAEB30TF PGA Carica papaya genomic clone PGAE30, genomic survey sequence.	COMMENT
ACCESSION	CG026604	Mueller Laboratory
VERSION	CG026604.1	Penn State University
KEYWORDS	GSS.	200 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn State University, University Park, PA 16802, USA
SOURCE	Carica papaya (papaya)	Tel: 814 863 6413
ORGANISM	Carica papaya	Fax: 814 865 9131
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroids II; Brassicales; Caricaceae; Carica.	Email: cwid3@psu.edu or jhl100@psu.edu	
REFERENCE	1 (bases 1 to 764)	The sequence provided is trimmed of vector and low quality regions.
AUTHORS	Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.	Full sequence and original trace file are available from the Plant Genome Network website ( <a href="http://pgn.cornell.edu">http://pgn.cornell.edu</a> )
TITLE	Whole genome shotgun sequencing of Carica papaya	Plate: Pam01-9ms1 row: a column: 06
JOURNAL	Unpublished (2003)	Seq primer: M13F.
COMMENT	Other GSS: PGAE30TR	Location/Qualifiers
FEATURES	Contact: Chris Town	source
source	TIGR	/organism="Persea americana"
	9712 Medical Center Drive, Rockville, MD 20850, USA.	/mol_type="mRNA"
	Tel: 301-833-3523	/db_xref="PGN:pam01-9ms1-a06"
	Fax: 301-838-0208	/clone="pam01-9ms1-a06"
	DNA provided by Ray Ming was isolated from cultivar Sunup that was transgenic for papaya ringspot virus coat protein gene	/tissue_type="flower buds"
	Seq primer: TF	/dev_stage="1-20 mm buds"
	Class: sheared ends.	/lab_host="SOLR"
	Location/Qualifiers	/clone_lib="Pam01"
	1. . 764	/note="vector: pBluescript SK (+/-; site 1: EcoRI; site 2: XbaI; This is a directionally cloned, non-normalized library. This library has been generated by the Floral Genome Project (fgp). The Floral Genome Project is funded by NSF's Plant Genome Research Program (DBI-0115884). More information about the project can be obtained at <a href="http://fgp.bio.psu.edu">http://fgp.bio.psu.edu</a> "
ORIGIN		
	Query Match Score 91.6; DB 10; length 764;	Query Match Score 91.2; DB 7; length 610;
	Best Local Similarity 85.1%; Pred. No. 6.7e-19;	Best Local Similarity 85.6%; Pred. No. 8.7e-19;
	Matches 114; Conservative 0; Mismatches 19; Indels 1; Gaps 1;	Matches 113; Conservative 0; Mismatches 18; Indels 1; Gaps 1;
QY	1 GCTCCCCCCCCTGGTCAATGAGAATGATGATAAGAGGCCCTGGATGACGTGAGGG 60	QY 1 GCTCCCCCCCCTGGTCAATGAGAATGATGATAAGAGGCCCTGGATGACGTGAGGG 60
Db	662 GCTCCCCCCCCTGGTCAATGAGAATGATGATAAGAGGCCCTGGATGACGTGAGGG 603	Db 48 GCTCCCCCCCCTGGTCAATGAGAATGATGATAAGAGGCCCTGGATGACGTGAGGG 107
QY	61 CAGGGATGCTATA - TCTGGGAGGAACTCCGGGATACCAAGCCTTGATACGT 119	QY 61 CAGGGATGCTATA - TCTGGGAGGAACTCCGGGCAATACGAAGGCGCTTGATACGT 119
Db	602 TAGGATGCTATATTCTGGGAGGAACTCCGGGATATGAGGCATGATACAG 543	Db 108 TAGGATGCTATATTCTGGGAGGAACTCCGGGATATGAGGCATGATACAG 167
QY	120 TGTAGGGAGGATT 133	QY 120 TGTAGGGAGGATT 131
Db	542 TTARGCCTTGTGAAT 529	Db 168 CCTTGGGATGAA 179
RESULT	8	RESULT 9
CK767400	CK767400	BH674012
LOCUS	610 bp mRNA	839 bp DNA
DEFINITION	linear EST 09-JUN-2005	linear
ACCESSION	pam01-9ms1-a06	GSS 19-FEB-2002
KEYWORDS	Pam01-9ms1-a06	BOMHD96TR BO 2-3 KB Brassica oleracea genomic clone BOMHD96,
ORGANISM	Persea americana (avocado)	genomic survey sequence.
VERSION	CK767400.1	BH674012
REFERENCE	CK767400.1 GI:42721434	BH674012.1 GI:18742175
AUTHORS	Persea americana (avocado)	Keywords
SOURCE		Brassica oleracea
ORGANISM	Persea americana (avocado)	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroids II; Brassicales; Brassicaceae; Brassica.
REFERENCE	1 (bases 1 to 839)	Reference Authors
AUTHORS	Eyle,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Utterback,T.R., Wostman,J.R., White,O.R. and Town,C.D.	Title
JOURNAL	Whole genome shotgun sequencing of <i>Brassica oleracea</i> and its application to gene discovery and annotation in <i>Arabidopsis</i> Genome Res. 15 (4), 487-495 (2005)	Comment
PUBLISHED	1580490	Contact: Chris Town
JOURNAL	Unpublished (2003)	TIGR
	9712 Medical Center Drive, Rockville, MD 20850, USA.	

		Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TR Class: sheared ends.
FEATURES	source	Location/Qualifiers 1. 839 /organism="Brassica oleracea" /mol_type="genomic DNA" /strain="TOL1000DH3" /db_xref="taxon:3712" /clone_id="BOMHD6" /clone_lib="SO_2_3 KB" /note="Vector: pho51; Site 1: BstX1; 2-3 kb sheared genomic DNA inserted into pho51 using BstX1 linkers"
ORIGIN		
Query Match		68.4%; Score 91; DB 9; Length 839;
Best Local Similarity		80.9%; Pred. No. 1.1e-18;
Matches	106; Conservative	0; Mismatches 25; Indels 0; Gaps 0;
QY	3	TCCCCCGCCGCGTCATGAGAATGGATAGAGGCTCGGGATTGACCTGAGGGCA 62
Db	828	TCTTCGGCTGTGATCGATAAGATAAGGATAGAGGCTCGGGATTGACCTGAGGGCA 769
QY	63	GGGATGGCTATATTCTGGGGGAACTCCGGGGATACGAGCCTGGATACAGTGT 122
Db	768	GGGGTAGCTATATTCTGGGGGAACTCCGGGGATACGAGCCTGGATACAGTGT 709
QY	123	AGGGAGGAGATT 133
Db	708	TGACTTGGAAAT 698
RESULT 10		
LOCUS	CN859023	00728AAA008805HT (AAAA) Royal Gala 59 DAFB fruit, Seeds removed
DEFINITION		380 bp mRNA linear EST 03-JUN-2004
ACCESSION	CN859023	Malus x domestica clone AAA008805, mRNA sequence.
VERSION	CN859023.1	GI:48114953
SOURCE		EST.
ORGANISM		Malus x domestica
REFERENCE		Bakryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; euroids I; Rosales; Maloideae; Malus.
AUTHORS		Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Jansen,B., McCartney,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y.
TITLE		Whole Genome Shotgun Reads from Brassica oleracea
JOURNAL		Published (2001)
COMMENT		Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory, T., Bal,H., Dedhia,N. and McCombie,W.R. PO Box 110, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8874 Fax: 516 367 8874 Email: mccombie@cshl.org Plate: eg27 row: e column: 02 Seq primer: -21fwdUniv Class: shotgun
FEATURES	source	High quality sequence stop: 491. Location/Qualifiers 1. 491 /organism="brassica oleracea" /mol_type="genomic DNA" /db_xref="taxon:3712" /clone="eg27e02" /clone_id="TOL1000DH3" /note="Vector: M13 for .x reads, pzero-2 for .b and .g reads; Site 1: EcoRV; DNA prepared as whole genome shotgun library from young, green leaves. May contain some plastid DNA. DNA provided by Dr. Tom Osborn, University of Wisconsin-Madison, Department of Agronomy."
FEATURES	source	Location/Qualifiers 1. 380 /organism="Malus x domestica" /mol_type="mRNA" /db_xref="taxon:3750" /clone="AAA008805" /tissue="fruit" /note="Vector: pBK-CMV. Library sequenced by Genesis Research & Development, Library sequenced by Genesis Research & Development"
ORIGIN		
Query Match		68.1%; Score 90.6; DB 7; Length 380;
Best Local Similarity		84.3%; Pred. No. 1.3e-18;
Matches	113; Conservative	0; Mismatches 20; Indels 1; Gaps 1;
QY	1	GCTCCCCCGCGTCATGAGAATGGATAGAGGCTCGGGATTGACCTGAGGG 60
Db	111	GCTCCCTCGCTGTGATCGATAAGATAAGGCTCGGGATTGACCTGAGGG 52
QY	61	CAGGGATGGCTATATTCTGGGGAACTCCGGGGATACGAGCCTG 111

Db	51 TAGGGTAGCTTATGGAGGCACTCCATCGAATATGAGCGCATG	1	REFERENCE Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 775)
RESULT	12	BZ511771	DEFINITION BOMQ22TR BO_2_3 KB Brassica oleracea genomic clone BOMQ22, LOCUS genomic survey sequence.
ACCESSION	BZ511771	JOURNAL GSS 16-DBC-2002	VERSION BZ511771.1 GI:27037291
KEYWORDS	GSS.	COMMENT	Other_GSS: BOMN79TF Contact: Chris Town
SOURCE	Brassica oleracea	ORGANISM	Brassica oleracea Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 770)
AUTHORS	Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D., Ayel, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Genome Res. 15 (4), 487-495 (2005)	TITLE	Whole genome shotgun sequencing of <i>Brassica oleracea</i> and its application to gene discovery and annotation in <i>Arabidopsis</i>
TITLE	utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D., application to gene discovery and annotation in <i>Arabidopsis</i>	JOURNAL	Genome Res. 15 (4), 487-495 (2005)
JOURNAL		PUBLISHED	15805490
PUBLISHED	15805490	COMMENT	Other_GSS: BOMN79TF Contact: Chris Town
COMMENT	Other_GSS: BOMQ22TP Contact: Chris Town	ORGANISM	TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtown@tigr.org
FEATURES	source	FEATURES	TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdtown@tigr.org
SOURCE		SOURCE	
FEATURES	location/Qualifiers	FEATURES	
LOCATION	sheared ends.	LOCATION	
1.	1..770	1.	
/mol_type="genomic DNA"	/organism="Brassica oleracea"	/mol_type="genomic DNA"	
/strain="TO000DH3"	/strain="TO1000DH3"	/strain="TO000DH3"	
/db_xref="Taxon:3712"	/clone_id="BOMN79"	/clone_id="BOMN79"	
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ORIGIN		ORIGIN	
Query Match	64.1%; Score 85.2; DB 9; Length 770;	Query Match	64.1%; Score 85.2; DB 9; Length 775;
Best Local Similarity	82.1%; Pred. No. 8.2e-17;	Best Local Similarity	82.1%; Pred. No. 8.2e-17;
Matches	110; Conservative 0; Mismatches 23; Indels 1; Gaps 1;	Matches	110; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
QY	1 GCTCCCCCGCGCTGTCATGAGATGATAGAGGCTCGTGGATGACGTGAGGG	QY	1 GCTCCCCCGCGCTGTCATGAGATGATAGAGGCTCGTGGATGACGTGAGGG
Db	5 GCTCCCTCGCTGCTGATGATGAGATGATGAGGCTCGTGGATGACGTGAGGG	Db	11 GCTCCCTCGCTGCTGATGAGATGATGAGGCTCGTGGATGACGTGAGGG
QY	61 CAGGGATGGCTATA-TCTGSGAGGAACTCCGGGGAATACGAGCCTCGGGCTTGATAGT	QY	61 CAGGGATGGCTATA-TCTGSGAGGAACTCCGGGGAATACGAGCCTCGGGCTTGATAGT
Db	65 TAGGGTAGCTTATTCGGGAGGCACTCCATCGGAATAGGCCATGGATACAG	Db	71 TAGGGTAGCTTATTCGGGAGGCACTCCATCGGAATAGGCCATGGATACAG
QY	120 TGTAGGGAGGATT 133	QY	71 TAGGGTAGCTTATTCGGGAGGCACTCCATCGGAATAGGCCATGGATACAG 130
Db	131 TTATGACTTGGAAAT 144	Db	
RESULT	14	RESULT	14
LOCUS	BH957918	LOCUS	BH957918
DEFINITION	odf83c05_b1_B.oleracea002	DEFINITION	odf83c05_b1_B.oleracea002
ACCESSION	BH957918	ACCESSION	BH957918
VERSION	BH957918.1 GI:23439145	VERSION	BH957918.1 GI:23439145
KEYWORDS	GSS.	KEYWORDS	GSS.
SOURCE	Brassica oleracea	SOURCE	Brassica oleracea
ORGANISM	Brassica oleracea	ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 731)
REFERENCE	Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.	REFERENCE	Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
AUTHORS	Whole genome shotgun reads from <i>Brassica oleracea</i>	AUTHORS	Unpublished (2002)
COMMENT	Contact: Richard K. Wilson	COMMENT	Contact: Richard K. Wilson
GENOME SEQUENCING CENTER	Washington University School of Medicine	GENOME SEQUENCING CENTER	Washington University School of Medicine
VERSION	BH424823.1 GI:17610551	VERSION	BH424823.1 GI:17610551
GSS		GSS	
SOURCE	Brassica oleracea	SOURCE	Brassica oleracea
ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	ORGANISM	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
COMMENT	Seq primer: -21upr forward	COMMENT	Seq primer: -21upr forward
Class: shotgun	Class: shotgun	Class: shotgun	Class: shotgun

High quality sequence start: 25  
 High quality sequence stop: 522.  
 Location/Qualifiers

FEATURES	source	ORIGIN
		total DNA inserted into phos1 using Bax1 linkers"
Query Match		origin
Best Local Similarity		Query Match
Matches 109; Conservative 0; Mismatches 24; Indels 1; Gaps 1		Score 62.9%; Score 83.6;
Qy 1. .713 /organism="Brassica oleracea"		DB 9; Length 183;
/mol_type="genomic DNA"		Accession B0A129R BO_1.6_2_KB_tot_Brassica_oleracea_genomic_clone_BO0A129,
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/clone_1b="B_oleracea002"		KEYWORDS GSS.
/note="Vector: pORTM3; Whole genome shotgun library from		SOURCE Brassica oleracea
flowering buds. DNA was purified from a crude nuclear		ORGANISM Brassica oleracea
prep using Brassica oleracea TO1000DH3 buds provided by		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Thomas Osborn at the University of Wisconsin. Genomic		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
DNA was provided by Pablo Raininowicz (CSHL) and the		rosids; eurosids II; Brassicales; Brassiceae; Brassica.
shotgun library prepared at Washington University Genome		REFERENCE 1 (bases 1 to 183)
Sequencing Center."		Aylee, N., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
RESULT 15 LOCUS B2483881 DEFINITION B0A129R BO_1.6_2_KB_tot_Brassica_oleracea_genomic_clone_BO0A129,		Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.
ACCESSION B2483881 VERSION B2483881.1 GI:26786279		Title Whole genome shotgun sequencing of Brassica oleracea and its
VERSION B2483881.1 GI:26786279		application to gene discovery and annotation in Arabidopsis
KEYWORDS GSS.		Journal Genome Res. 15 (4), 487-495 (2005)
SOURCE Brassica oleracea		PUBMED 1580590
ORGANISM Brassica oleracea		COMMENT Other GSS: BO0A129T
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		Contact: Chris Town
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;		TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
rosids; eurosids II; Brassicales; Brassiceae; Brassica.		Tel: 301-838-3523
REFERENCE 1 (bases 1 to 183)		Fax: 301-838-3208
Aylee, N., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,		Email: catown@tigr.org
Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.		DNA is from a doubled haploid provided by Tom Osborn.
Title Whole genome shotgun sequencing of Brassica oleracea and its		Seq primer: TR
Journal Genome Res. 15 (4), 487-495 (2005)		Class: sheared ends.
PUBMED 1580590		FEATURES source
COMMENT Other GSS: BO0A129T		Location/Qualifiers
Contact: Chris Town		1. .183 /organism="Brassica oleracea"
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.		/mol_type="genomic DNA"
Tel: 301-838-3523		/strain="TO1000DH3"
Fax: 301-838-3208		/db_xref="taxon:3712"
Email: catown@tigr.org		/clone="BO0A129"
DNA is from a doubled haploid provided by Tom Osborn.		/clone_1b="BO_1.6_2_KB_tot"
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Class: sheared ends.		note=pORTM3;"

“rage Blank (uspto)

GenCore version 5.1.7  
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Om nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:31:51 ; Search time 485 Seconds

(without alignments)

1827.637 Million cell updates/sec

Title: US-10-663-241-32  
Perfect score: 133

Sequence: 1 gtcgcggccgtcgatca.....tacagtgttagggaggatt 133

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_21:  
1: geneseqn1980s:  
2: geneseqn1990s:  
3: geneseqn2000s:  
4: geneseqn2001as:  
5: geneseqn2001bs:  
6: geneseqn2002as:  
7: geneseqn2002bs:  
8: geneseqn2003as:  
9: geneseqn2003bs:  
10: geneseqn2003cs:  
11: geneseqn2003ds:  
12: geneseqn2004as:  
13: geneseqn2004bs:  
14: geneseqn2005s:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description	RESULT 1
1	133	100.0	133	2	AAX95999	AAV99599 standard; DNA; 133 BP.	AAV99599
2	122	91.7	165	2	AAX21409	RPRN_PEP	PR
3	122	91.7	168	2	AAX21407	RAX21407_PRRN_PRC1	PR
4	122	91.7	176	12	ADM01882	Adm01882_Plasmid_1	XX
5	122	91.7	1134	2	AAT85195	At85195_Plasmid_t	XX
6	122	91.7	1134	2	AAX21415	RAX21415_Selectable	XX
7	122	91.7	1143	10	ADE06202	Nicotiana	XX
8	122	91.7	9148	12	AD085784	Ado85784_Chimeric	XX
9	122	91.7	1332	12	AD085782	Ado85782_Chimeric	XX
10	122	91.7	1416	2	AAX21432	Aax21432_Regulator	XX
11	122	91.7	1417	2	AAX21423	Aat85196_Plasmid_t	XX
12	122	91.7	1417	10	AD06203	Ado6203_Plasmid_t	XX
13	91.7	91.7	5834	12	ADM01293	Adm01293_Plasmid_p	XX
14	91.7	91.7	6465	12	ADM01293	Adm01293_Plasmid_p	XX
15	91.7	6659	12	ADM01290	Adm01290_Plasmid_p	XX	
16	91.7	7549	12	ADM01292	Adm01292_Plasmid_p	XX	
17	91.0	161	2	AAX21423	Aax21423_5' and 3'	CC	
18	91.0	1183	3	AAX21376	Aax61376_Nucleotid	CC	
19	91.0	1208	2	AAX21433	Aax21433_Regulator	CC	

Disclosure: Page 4; 79pp; English.

This is the nucleotide sequence of plasmid-encoded plastid RNA polymerase (PEP). Prrn promoter elements (See AAV9569-99) or homologues are used for producing exogenous proteins of interest in plant plastids. Also new is a DNA construct for

CC stably transforming the plasmids of higher plants comprising: (i) a transcription unit encoding at least one exogenous protein of interest, and (ii) a first nuclear-encoded plastid (NEP) RNA polymerase promoter, and a second PEP RNA polymerase promoter in tandem operably linked to the transcription unit, where expression of the transcription unit is regulated by the promoters. Use of the novel constructs facilitates transformation of a wide range of plant species, allowing ubiquitous expression of a transforming DNA in plasmids (e.g., chloroplasts) of multicellular plants. Preferred promoter combinations are the *Prnr* PEP promoters combined with clPP type II NEP promoter in dicots and the *Prnr* PEP promoter combined with the clPP type II NEP promoter in monocots and dicots. (Updated on 27-AUG-2003 to correct OS field.)

SQ Sequence 133 BP; 30 A; 25 C; 50 G; 28 T; 0 U; 0 Other;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-37;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCCCGCGCGTCGTCAATCAGAATGGATAGAGGCTCTGGGATTGACGTAGGGGG 60  
 Db 1 GCTCCCCCGCGCGTCGTCAATCAGAATGGATAGAGGCTCTGGGATTGACGTAGGGGG 60

Qy 61 CAGGGATGGCTATACTCTGGAGGGAATCCGGGCCATAGGAGGCCTTGATACAGTT 120  
 Db 61 CAGGGATGGCTATACTCTGGAGGGAATCCGGGCCATAGGAGGCCTTGATACAGTT 120

Qy 121 GTAGGGAGGATT 133  
 Db 121 GTAGGGAGGATT 133

RESULT 2  
 AAX21409  
 ID AAX21409 standard; DNA; 165 BP.  
 XX  
 AC AAX21409;  
 DT 21-MAY-1999 (first entry)  
 DE *Prrn* promoter sequence.  
 XX  
 KW Construct; marker; antibiotic resistance; regulatory sequence; promoter;  
 KW stabilizing sequence; plastid; plant; ss.  
 OS Synthetic.  
 OS Nicotiana tabacum.  
 XX  
 PN US5877402-A.  
 XX  
 PR 01-MAY-1990; 90US-00518763.  
 PR 25-AUG-1993; 93US-00111398.  
 XX  
 PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
 XX  
 PI Maliga ZS, Maliga P, Staub JM;  
 XX  
 PR 02-MAR-1999.  
 XX  
 PP 31-JAN-1994; 94US-00189256.  
 PR 01-MAY-1990; 90US-00518763.  
 PR 25-AUG-1993; 93US-00111398.

XX  
 PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.  
 XX  
 PR 1999-189744/16.

XX  
 PT New DNA construct containing an antibiotic resistance marker - useful for stably transforming the plasmids of multicellular plants.  
 XX  
 PS Disclosure; Fig 8; 101pp; English.

XX  
 CC The invention relates to a DNA construct, containing a non-lethal stable marker (e.g. antibiotic resistance) under the control of a 5' regulatory sequence and a 3' stabilizing sequence, for stably transforming the plasmids of multicellular plants and allowing expression of heterologous proteins especially non-native plastid or plant proteins. This sequence corresponds to the regulatory region of the plasmid pRN32 and comprises the 16S ribosomal RNA operon promoter (*Prrn*), the rbcL leader sequence including the ribosome binding site and the first 5 amino acids coding sequence from the ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (Rubisco) gene.

XX  
 SQ Sequence 168 BP; 44 A; 32 C; 57 G; 35 T; 0 U; 0 Other;  
 CC sequence 91.7%; Score 122; DB 2; Length 168;  
 CC Best Local Similarity .99.3%; Pred. No. 2.9e-33;  
 CC Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGGGCTTCAATGAGATGGATAAGGGCTGGGATTCAGCTGAGGGG 60  
 QY 1 GCTCCCCCGGGCTTCAATGAGATGGATAAGGGCTGGGATTCAGCTGAGGGG 60  
 Db 1 GCTCCCCCGGGCTTCAATGAGATGGATAAGGGCTGGGATTCAGCTGAGGGG 60  
 QY 61 CAGGGATGGCTATA-TTCGGGACGGAACTCCGGGAAATCGAGGCCTGAGTACAGT 119  
 Db 61 CAGGGATGGCTATA-TTCGGGACGGAACTCCGGGAAATCGAGGCCTGAGTACAGT 119  
 QY 120 TGTAGGGAGGGATT 133  
 Db 121 TGTAGGGAGGGATT 134  
 QY 136 TGTAGGGAGGGATT 149

**RESULT 4**

ADM01282  
 ID ADM01282 standard; DNA; 176 BP.  
 XX AC  
 XX AC  
 XX DT 01-JUL-2004 (first entry)

**Plastid 16S ribosomal RNA subunit promoter sequence.**

KW vector; plastid; artificial intergene region; plant;  
 KW transplastomic angiosperm; agronomic property; stress resistance;  
 KW rbcL gene; ds.  
 OS Unidentified.

XX PN WO2004029256-A2.

XX PD 08-APR-2004.

XX PP 15-SEP-2003; 2003WO-CU0000009.

XX PR 27-SEP-2002; 2002CU-00000208.  
 XX PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.

XX PI Selman-Housein Sosa G, Aguiar Cabeza B, Gonzalez Quintero ADC;  
 PI Ramos Gonzalez O;

XX DR WPI; 2004-316131/29.

**DNA vector for transformation and expression in plastids, useful e.g. for producing pharmaceutical proteins or improving agronomic properties, having gene inserted in artificial intergene region.**

XX PS Example 1; SEQ ID NO 14; 74PP; Spanish.

XX CC The invention relates to a DNA vector (A) for stable transformation and expression of genes (I) in plastids, where (I) is inserted in an artificial intergene region (AIR) formed by combining two 5'-untranslated regions (5'-UTRs) of genes that transcribe in different directions and are derived from plants of different divisions or classes. (A) are used to produce transplastomic angiosperms that have improved agronomic properties (e.g. resistance to biotic or abiotic stress) or express a very wide range of agricultural, veterinary, pharmaceutical, nutritional or industrial products, e.g. enzymes, vaccines, antibiotics, cytokines or immunoglobulins. Use of (A) eliminates the need for a transposon for gene insertion, inserted genes do not require promoter and terminators, and the structure of flanking sequences in (A) ensures universal applicability. Also any selection marker in (A) can be eliminated by homologous recombination. (A) provides efficient and stable expression of genes without causing any functional alterations. This sequence represents the plastid 16S ribosomal RNA subunit promoter sequence used to generate the vectors of the invention.

XX Sequence 176 BP; 39 A; 37 C; 60 G; 40 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 12; Length 176;  
 Best Local Similarity 99.3%; Pred. No. 2.9e-33;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 GCTCCCCCGGGCTTCAATGAGATGGATAAGGGCTGGGATTCAGCTGAGGGG 60  
 QY 16 GCTCCCCCGGGCTTCAATGAGATGGATAAGGGCTGGGATTCAGCTGAGGGG 60  
 Db 61 CAGGGATGGCTATA-TTCGGGACGGAACTCCGGGAAATCGAGGCCTGAGTACAGT 119  
 QY 76 CAGGGATGGCTATA-TTCGGGACGGAACTCCGGGAAATCGAGGCCTGAGTACAGT 119  
 Db 76 CAGGGATGGCTATA-TTCGGGACGGAACTCCGGGAAATCGAGGCCTGAGTACAGT 135  
 QY 120 TGTAGGGAGGGATT 133  
 Db 120 TGTAGGGAGGGATT 133

**RESULT 5**

AAT85195/c ID AAT85195 standard; DNA; 1134 BP.

XX AC  
 XX DT 10-MAR-1998 (first entry)

**Plastid targeting region of plasmid pGS31A.**

KW Plastid; transformation; transplastomic plant; transgenic plant;  
 KW Brassica; cruciferous plant; vector; Plasmid pGS31A;  
 KW spectinomycin resistance; Selectable marker; ada gene; ss.  
 OS Arabidopsis thaliana.  
 OS Synthetic.  
 OS Chimeric.

XX PN WO9732377-A1.

XX PD 12-SEP-1997.

XX PF 06-MAR-1997; 97WO-US003444.

XX PR 06-MAR-1996; 96US-0012916P.

XX PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

XX DR Maliga P, Sikdar SR, Reddy SV;

XX PT Production of transplastomic plants - by transfection with Plastid targeted DNA, specifically for Cruciferous plants.

XX PS Disclosure; Fig 6; 45pp; English.

XX CC This sequence comprises the plastid targeting region of plasmid pGS31A. This plasmid carries a spectinomycin resistance gene (ada) flanked by Arabidopsis plastid DNA sequences that target its insertion between trnV and the rps 12/7 operon. It was produced by ligating the chimeric ada gene from Ecl1261II into the unique HincII site of plasmid pGS7 (see AAT85194). A novel method of production of transplastomic plants involves: delivering transforming DNA, preferably cloned in pGS31A, pGS85A or pGS7, to a plastid genome of plant cells in culture, selecting cells with transformed plastids and regenerating these to plants. The transforming DNA comprises (i) (i) several targeting sequences (i.e. plastid DNA sequences from the genome to be transformed to allow homologous recombination, (ii) 5' and 3' regulatory regions from plastid DNA linked to an antibiotic resistance gene for use as selection marker, (iii) similar regulatory regions controlling a foreign gene of interest, and (iv) at least one cloning site for insertion of the foreign gene adjacent to the marker gene. The method is used to transform cruciferous plants, e.g. Brassica species. The combination of homologous recombination, selectable marker and use of plastid regulatory sequences improves generation of stably transformed plants. Expression of foreign genes in plastids, rather than in the nucleus, avoids risk of transmitting the foreign gene in the pollen, provides high levels of

CC protein expression, permits simultaneous incorporation of several genes and avoids the positional effects and gene silencing associated with nuclear transformation

XX Sequence 1134 BP; 295 A; 310 C; 248 G; 281 T; 0 U; 0 Other; Best Local Similarity 91.7%; Score 122; DB 2; Length 1134; Matches 133; Conservative 99.3%; Pred. No. 5.2e-33; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCCCTCGTCATGAGAATTGATAGAGGCTCTGGGATGAGCTGGGG 60 Db 1130 GCTCCCCCGCCCTCGTCATGAGAATTGATAGAGGCTCTGGGATGAGCTGGGG 1071 QY 61 CAGGGATGGCTATA-TTCTGGCAGCGACTCTGGGCAATACGAACCGCTTGATACGT 119 Db 998 CAGGGATGGCTATA-TTCTGGCAGCGACTCTGGGCAATACGAACCGCTTGATACGT 939

QY 120 TCTAGGAGGAGATT 133 Db 1010 TCTAGGAGGAGATT 997

RESULT 6 AAX21415/C

ID AAX21415 Standard; DNA; 1134 BP.

XX AC AAX21415;

XX DT 21-MAY-1999 (first entry)

DE Selectable marker gene for plasmid pPRV112A.

XX KW Construct; marker; antibiotic resistance; regulatory sequence; promoter; stabilizing sequence; plastid; plant; ss.

XX OS Synthetic.

XX US5877402-A.

XX PD 02-MAR-1999.

XX PP 31-JAN-1994; 94US-00189256.

XX PR 01-MAY-1990; 90US-00518763.

XX PR 25-AUG-1993; 93US-00111398.

XX PA (RUTF ) UNIV RUTGERS STATE NEW JERSEY.

PI Maliga ZS, Maliga P, Staub JM;

XX DR WPI; 1999-18974/16.

PT New DNA construct containing an antibiotic resistance marker - useful for stably transforming the plastids of multicellular plants.

XX PS Claim 21; Fig 20E; 101pp; English.

The invention relates to a DNA construct, containing a non-lethal stable marker (e.g. antibiotic resistance) under the control of a 5' regulatory sequence and a 3' stabilizing sequence, for stably transforming the plastids of multicellular plants and allowing expression of heterologous proteins especially non-native plastid or plant proteins. This sequence corresponds to the selectable marker gene for the plasmid pPRV112A.

XX Sequence 1134 BP; 291 A; 303 C; 257 G; 283 T; 0 U; 0 Other; Query Match 91.7%; Score 122; DB 2; Length 1134; Best Local Similarity 99.3%; Pred. No. 5.2e-33; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCCCTCGTCATGAGAATTGATAGAGGCTCTGGGATGAGCTGGGG 60 Db 1058 GCTCCCCCGCCCTCGTCATGAGAATTGATAGAGGCTCTGGGATGAGCTGGGG 999 QY 61 CAGGGATGGCTATA-TTCTGGCAGCGACTCTGGGCAATACGAACCGCTTGATACGT 119 Db 998 CAGGGATGGCTATA-TTCTGGCAGCGACTCTGGGCAATACGAACCGCTTGATACGT 939

RESULT 7 ADE06202/C

ID ADE06202 Standard; DNA; 1143 BP.

XX AC ADE06202;

XX DT 29-JAN-2004 (first entry)

DE Nicotiana tabacum targeting region of plasmid pGS31A.

XX OS Nicotiana tabacum.

XX DN US20031200568-A1.

XX BD 23-OCT-2003.

XX PP 12-JUN-2003; 2003US-00460716.

XX PR 06-MAR-1997; 97W0-US0033444.

PR 05-FEB-1999; 99US-00142114.

PR 13-MAR-2000; 2000US-00524087.

XX PA (MALI/) MALIGA P.

PA (SKAR/) SKARJINSKAIA M.

PA (MALI/) MALIGA Z S.

PI Maliga P, Skarjinskaia M, Maliga ZS;

XX DR WPI; 2003-852834/79.

XX PT New improved vector for transforming plastids of higher plants and comprising a targeting segment having first and second chimeric targeting sequences, useful for creating transplastomic plants.

XX PS Disclosure; SEQ ID NO 2; 35pp; English.

The present invention relates to a new improved vector (pZS391B) for transforming plastids of higher plants. The vector comprises a targeting segment having first and second chimeric targeting sequences for facilitating recombination within the plastid genome, each of which flanks at least one transgene of interest and has a first portion derived from the plant species being targeted for transformation, and a second portion derived from a different plant species. The transgene constitutes a monoclonal or polyclonal expression unit comprising a selectable marker gene and a foreign gene of interest. It encodes a selectable marker, herbicide resistance or drought resistance gene. The selectable marker gene comprises kanamycin, streptomycin or spectinomycin. The plastids are chloroplasts. The vector is useful for transforming plastids of higher plants (e.g. Brassica plants), and for creating transplastomic plants. The methods and compositions of the invention facilitate the regeneration of transformed plants following the delivery of beneficial DNA molecules. The present sequence represents Nicotiana tabacum targeting region of plasmid pGS31A.

XX Sequence 1143 BP; 297 A; 313 C; 252 G; 281 T; 0 U; 0 Other; Query Match 91.7%; Score 122; DB 10; Length 1143; Best Local Similarity 99.3%; Pred. No. 5.2e-33; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Matches	133;	Conservative	0;	Mismatches	0;	Indels	1;	Gaps	1;
QY	1	GCTTCCCCCGCTGCTTCATGAGATGTTAAGGGCTGCTGGATGAGCTGAGGGCG	60						
Db	1130	GCTTCCCCCGCTGCTTCATGAGATGTTAAGGGCTGCTGGATGAGCTGAGGGCG	1071						
QY	61	CAGGGATGCTATA-TTCGGGACCGAACTCCGGGATAACGAGCTGGATTGAGTGAGGGCG	119						
Db	1070	CAGGGATGCTATA-TTCGGGACCGAACTCCGGGATAACGAGCTGGATTGAGTGAGGGCG	1011						
QY	120	TGTAGGGAGGGATT 133							
Db	1010	TGTAGGGAGGGATT 997							

**RESULT 8**

Matches	133;	Conservative	0;	Mismatches	0;	Indels	1;	Gaps	1;
QY	1	GCTTCCCCCGCTGCTTCATGAGATGTTAAGGGCTGCTGGATGAGCTGAGGGCG	60						
Db	1	GCTTCCCCCGCTGCTTCATGAGATGTTAAGGGCTGCTGGATGAGCTGAGGGCG	60						
QY	61	CAGGGATGCTATA-TTCGGGACCGAACTCCGGGATAACGAGCTGGATTGAGTGAGGGCG	119						
Db	61	CAGGGATGCTATA-TTCGGGACCGAACTCCGGGATAACGAGCTGGATTGAGTGAGGGCG	120						
QY	120	TGTAGGGAGGGATT 133							
Db	121	TGTAGGGAGGGATT 134							

**RESULT 9**

ADO85784  
ID ADO85784 standard; DNA; 1148 BP.

XX  
AC  
XX  
ADO85784;

XX  
DT 09-SEP-2004 (first entry)

XX  
DB

Chimeric gene AADA-129 SEQ ID NO:3.

XX  
KW ds; gene; elementary chimeric gene; hydroxyphenyl pyruvate dioxygenase;

KW HPPD; plant; weed control; herbicide.

XX  
OS Nicotiana tabacum.

OS ChimERIC.

XX  
FH  
FT CDS  
FT /\*tag= a  
FT /product= "AADA-129"

XX  
PN FR2848568-A1.

XX  
PD 18-JUN-2004.

XX  
PR 17-DEC-2002; 2002FR-00015975.

XX  
PA (RHOB-) RHOBIO SA.

XX  
PT Tissot G, Wisniewski JP, Ferullo JM;

XX  
PI DR WPI; 2004-452915/43.

DR P-PSDB; ADO85785.

XX  
PS Example 1; SEQ ID NO 3; 47pp; French.

XX  
PT New chimeric gene including a sequence for hydroxyphenyl pyruvate dioxygenase, useful for preparing transgenic plants resistant to herbicides that target this enzyme, by plastid transformation.

XX  
PS Example 1; SEQ ID NO 1; 47pp; French.

XX  
PT New chimeric gene including a sequence for hydroxyphenyl pyruvate dioxygenase, useful for preparing transgenic plants resistant to herbicides that target this enzyme, by plastid transformation.

XX  
PS Example 1; SEQ ID NO 1; 47pp; French.

XX  
PT The invention relates to a novel chimeric gene (CG) comprising at least one elementary chimeric gene (eCG) that consists of, functionally linked in the direction of transcription, a promoter (P), functional in plants, a sequence encoding hydroxyphenyl pyruvate dioxygenase (HPPD) and a terminator, functional in plants. The chimeric genes of the invention are used to impart resistance to herbicides that target HPPD, so that plants containing CG can be safely treated, for weed control, with these herbicides. Plastid transformation, which involves a double homologous recombination, is precisely targeted, avoiding positional effects that occur during nuclear transgenesis. The present sequence represents an elementary chimeric gene of the invention.

XX  
SQ Sequence 1148 BP; 314 A; 256 C; 307 G; 271 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 12; Length 1148;

Best Local Similarity 99.3%; Pred. No. 5.2e-33;

Query Match 91.7%; Score 122; DB 12; Length 1332;

Best Local Similarity 99.3%; Pred. No. 5.4e-33;

Matches	Db	133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY	1	GTCGCCCGCCGCTGGTCAATGAGATGGATAAGGGCTGTGGGATGACGTGGGGG 60
Db	1	GTCGCCCGCCGCTGGTCAATGAGATGGATAAGGGCTGTGGGATGACGTGGGGG 60
QY	61	CAGGGATGCCTATAATTCTGGAGGGAACCTCGGGCGAATACGAGACGCTTGATACAGT 119
Db	61	CAGGGATGCCTATAATTCTGGAGGGAACCTCGGGCGAATACGAGACGCTTGATACAGT 120
QY	120	TGTAGGAGGGATT 133
Db	121	TGTAGGAGGGATT 134
RESULT 10		
AAX21432		
ID		AAX21432 standard; DNA; 1416 BP.
XX		
AC		AAX21432;
XX		
DT		21-MAY-1999 (first entry)
XX		
DE		Regulatory region Prn(L)/rbcl(S)/kan/Tpsba(L).
KW		Construct; marker; antibiotic resistance; regulatory sequence; promoter; stabilizing sequence; plastid; plant; ss.
XX		
OS		Synthetic.
XX		
PN		US5877402-A.
PD		02-MAR-1999.
PP		31-JAN-1994; 94US-00109256.
PR		01-MAY-1990; 90US-00518763.
PR		25-AUG-1993; 93US-00111398.
PA		(RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX		
PI		Maliga ZS, Maliga P, Staub JM;
PT		WPI; 1999-189744/16.
PT		New DNA construct containing an antibiotic resistance marker - useful for stably transforming the plastids of multicellular plants.
PS		Disclosure; Fig 2B; 101pp; English.
PT		The invention relates to a DNA construct, containing a non-lethal stable marker (e.g. antibiotic resistance) under the control of a 5' regulatory sequence and a 3' stabilizing sequence, for stably transforming the plastids of multicellular plants and allowing expression of heterologous proteins especially non-native plastid or plant proteins. This sequence corresponds to the regulatory region Prn(L)/rbcl(S)/kan/Tpsba(L) from the plasmid pRNH7
XX		
XX		Sequence 1416 BP; 312 A; 322 C; 379 G; 403 T; 0 U; 0 Other;
XX		Best Local Similarity 99.3%; Pred. No. 5.56-33; Score 122; DB 2; Length 1416; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY	1	GTCGCCCGCCGCTGGTCAATGAGATGGATAAGGGCTGTGGGATGACGTGGGGG 60
Db	22	GTCGCCCGCCGCTGGTCAATGAGATGGATAAGGGCTGTGGGATGACGTGGGGG 81
QY	61	CAGGGATGCCTATAATTCTGGAGGGAACCTCGGGCGAATACGAGACGCTTGATACAGT 119
Db	82	CAGGGATGCCTATAATTCTGGAGGGAACCTCGGGCGAATACGAGACGCTTGATACAGT 141
QY	120	TGTAGGAGGGATT 133
RESULT 11		
AT83196		
ID		AT83196 standard; DNA; 1417 BP.
XX		
AC		AT83196;
XX		
DT		10-MAR-1998 (first entry)
XX		
DE		Plastid targeting region of plasmid pGS85A.
KW		Plastid; transformation; transplastomic plant; transgenic plant; Brassica; cruciferous plant; vector; plasmid pGS85A;
KW		kanamycin resistance; neomycin phosphotransferase; neo gene; selectable marker; ss.
XX		
OS		Arabidopsis thaliana.
OS		Synthetic.
XX		
PN		Arabidopsis thaliana.
XX		
FH		Key
FT		Location/Qualifiers
FT		158 .970
FT		/*tag= a
FT		/note= "kanamycin resistance gene"
FT		
PN		W0932977-A1.
PD		12-SEP-1997.
XX		
PP		06-MAR-1997; 97WO-US003444.
XX		
PR		06-MAR-1996; 96US-0012916P.
XX		
PA		(RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX		
PI		Maliga P, Sikdar SR, Reddy SV;
XX		
DR		WPI; 1997-470593/43.
XX		
PT		Production of transplastomic plants - by transfection with plastid targeted DNA, specifically for Cruciferous plants.
XX		
PS		Disclosure; Fig 7; 45pp; English.
XX		
CC		This sequence comprises the plastid targeting region of plasmid pGS85A. This plasmid carries a neomycin phosphotransferase (neo) gene that confers kanamycin resistance gene, flanked on both sides by Arabidopsis plastid targeting sequences. It was produced by ligating the neo gene into the unique BlnII site of plasmid pGS7 (see AT85194). A novel method of producing transplastomic plants involves: delivering transforming DNA, preferably cloned in pGS3IA, pGS85A or pGS7, to a plastid genome of plant cells in culture, selecting cells with transformed plastids and regenerating these to plants. Transforming DNA comprises (i) (ii) several targeting sequences (i.e. plastid DNA sequences from the genome to be transformed) to allow homologous recombination, (iii) 5' and 3' regulatory regions from plastid DNA linked to a selectable marker gene, (iv) regulatory regions controlling a foreign gene of interest, and (iv) at a cloning site for insertion of the foreign gene adjacent to the marker gene. The method is used to transform cruciferous plants, e.g. Brassica species. The combination of homologous recombination, selectable marker and use of plastid regulatory sequences improves generation of stably transformed plants. Expression of foreign genes in plastids, rather than in the nucleus, avoids risk of transmitting the foreign gene in the pollen, provides high levels of protein expression, permits simultaneous incorporation of several genes and avoids the positional effects and gene silencing associated with nuclear transformation.
CC		Sequence 1417 BP; 312 A; 323 C; 379 G; 403 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 2; Length 1417;  
Best Local Similarity 90.3%; Pred. No. 5.5e-33; 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTCITCAATGAGATGGTAGAGGTCTGGGATGACGTTAGGGGG 60  
Db 23 GCTCCCCCGCGTCITCAATGAGATGGTAGAGGTCTGGGATGACGTTAGGGGG 60  
QY 61 CAGGGATGCTATA-TTCGGGAGGAATCCCGGAAATACGAGGCTTGAGTACAGT 119  
Db 83 CAGGGATGCTATA-TTCGGGAGGAATCCCGGGAATACGAGGCTTGAGTACAGT 142  
QY 120 TGTAGGGAGGGATT 133  
Db 143 TGTAGGGAGGGATT 156

RESULT 12

ADE06203  
ID ADE06203 standard; DNA; 1417 BP.  
XX  
AC  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Plastid targeting region of plasmid pGS85A.  
XX  
KW Brassica plant; plastid transformation; higher plant; transgene;  
KW plasmid pGS85A; ds.  
XX  
OS Unidentified.  
XX  
PN US2003200568-A1.  
XX  
PD 23-OCT-2003.  
XX  
PF 12-JUN-2003; 2003US-00460716.  
XX  
PR 06-MAR-1997; 97WO-US003444.  
PR 05-FEB-1999; 99US-00142114.  
PR 13-MAR-2000; 2000US-00524087.  
XX  
PA (MALI/) MALIGA P.  
PA (SKAR/) SKARJINSKAIA M.  
PA (MALI/) MALIGA Z S.  
XX  
PI Maliga P., Skarjinskaia M., Maliga ZS;  
DR WPI; 2003-852834/79.

XX  
PT New improved vector for transforming plastids of higher plants and  
PT comprising a targeting segment having first and second chimeric targeting  
PT sequences, useful for creating transplastomic plants.  
XX  
PS Disclosure; SEQ ID NO 3; 35pp; English.

XX  
The present invention relates to a new improved vector (pZS391B) for  
CC transforming plastids of higher plants. The vector comprises a targeting  
CC segment having first and second chimeric targeting sequences for  
CC facilitating recombination within the plastid genome, each of which  
CC flanks at least one transgene of interest and has a first portion derived  
CC from the plant species being targeted for transformation, and a second  
CC portion derived from a different plant species. The transgene constitutes  
CC a monocistronic or polycistronic expression unit comprising a selectable  
CC marker gene and a foreign gene of interest. It encodes a selectable  
CC marker, herbicide resistance or drought resistance gene. The selectable  
CC marker gene comprises kanamycin, streptomycin or spectinomycin. The  
CC plastids are chloroplasts. The vector is useful for transforming plastids  
CC of higher plants (e.g. Brassica plants), and for creating transplastomic  
CC plants. The methods and compositions of the invention facilitate the  
CC regeneration of transformed plants following the delivery of beneficial  
CC DNA molecules. The present sequence represents the plastid targeting  
CC

CC region of plasmid pGS85A.

CC region of plasmid pGS85A.

Query Match 91.7%; Score 122; DB 10; Length 1417;  
Best Local Similarity 90.3%; Pred. No. 5.5e-33; 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GCTCCCCCGCGTCITCAATGAGATGGTAGAGGTCTGGGATGACGTTAGGGGG 60  
Db 23 GCTCCCCCGCGTCITCAATGAGATGGTAGAGGTCTGGGATGACGTTAGGGGG 60  
QY 61 CAGGGATGCTATA-TTCGGGAGGAATCCCGGAAATACGAGGCTTGAGTACAGT 119  
Db 83 CAGGGATGCTATA-TTCGGGAGGAATCCCGGGAATACGAGGCTTGAGTACAGT 142  
QY 120 TGTAGGGAGGGATT 133  
Db 143 TGTAGGGAGGGATT 156

RESULT 13

ADM01283 standard; DNA; 5834 BP.  
XX  
AC ADM01283;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Plasmid pVTPA DNA sequence.  
XX  
KW vector; plastid; artificial intergene region; plant; stress resistance;  
KW rboL gene; ds.  
XX  
OS Synthetic.  
XX  
PN WO2004029256-A2.  
XX  
PD 08-APR-2004.  
XX  
PR 15-SEP-2003; 2003WO-CU0000009.  
XX  
PR 27-SEP-2002; 2002CU-00000208.  
XX  
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.  
XX  
PI Selman-Housein Sosa G., Aquilar Cabeza E., Gonzalez Quintero ABC;  
PI Ramos Gonzalez O;  
XX  
DR WPI; 2004-316131/29.  
XX  
DNA vector for transformation and expression in plastids, useful e.g. for  
PT producing pharmaceutical proteins or improving agronomic properties, has  
PT gene inserted in artificial intergene region.  
XX  
PS Example 1; SEQ ID NO 15; 74pp; Spanish.

The invention relates to a DNA vector (A) for stable transformation and  
CC expression of genes (1) in plastids, where (1) is inserted in an  
artificial intergene region (AIR) formed by combining two 5'-untranslated  
regions (5'-UTR) of genes that transcribe in different directions and  
CC are derived from plants of different divisions or classes. (A) are used  
CC to produce transplastomic angiosperms that have improved agronomic  
properties (e.g. resistance to biotic or abiotic stress), or express a  
CC very wide range of agricultural, veterinary, pharmaceutical, nutritional  
CC or industrial products, e.g. enzymes, vaccinating antigens, cytokines or  
CC immunoglobulins. Use of (1) eliminates the need for a transposon for gene  
CC insertion; inserted genes do not require promoters and terminators; and  
CC the structure of flanking sequences in (A) ensures universal  
CC applicability. Also any selection marker in (1) can be eliminated by  
CC homologous recombination. (A) provides efficient and stable expression of  
genes without causing any functional alterations. This sequence

CC represent an example of the vector of the invention.

XX SQ Sequence 5834 BP; 1586 A; 1288 C; 1402 G; 1558 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 12; Length 5834; Best Local Similarity 99.3%; Pred. No. 8; Se-33; Mismatches 0; Indels 1; Gaps 1;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 91.7%; Score 122; DB 12; Length 6465; Best Local Similarity 99.3%; Pred. No. 8; Se-33; Mismatches 0; Indels 1; Gaps 1;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GCTGCCCGCCGCGTGTCAATGAAATGAGGCTGGGATTGACCTGACGGGG 60  
Db 1918 GCTGCCCGCCGCGTGTCAATGAAATGAGGCTGGGATTGACCTGACGGGG 1977

Qy 61 CAGGGATGGCTATA-TCTGGAGGCACTCGGGCATAAGAGGCTTGATACGT 119  
Db 1978 CAGGGATGGCTATA-TCTGGAGGCACTCGGGCATAAGAGGCTTGATACGT 2037

Qy 120 TGTAGGGAGGATT 133  
Db 2038 TGTAGGGAGGATT 2051

RESULT 14

ADM01293 standard; DNA; 6465 BP.

ID ADM01293

AC XX

DT 01-JUL-2004 (first entry)

DE Plasmid pVT1PA-Bar DNA sequence.

KW vector; plastid; artificial intergene region; plant; transplastomic angiosperm; agronomic property; stress resistance; rbcl gene; ds.

OS Unidentified.

XX WO2004029256-A2.

XX PD 08-APR-2004.

PP 15-SEP-2003; 2003WO-CU0000009.

PR 27-SEP-2002; 2002CU-00000208.

PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.

PT Selman-Housein Sosa, G., Aguilar Cabeza, E., Gonzalez Quintero ADC;  
PI Ramos Gonzalez O;  
XX DR WPI; 2004-316131/29.

PT DNA vector for transformation and expression in plastids, useful e.g. for producing pharmaceutical proteins or improving agronomic properties, has gene inserted in artificial intergene region.

PS Example 9; SEQ ID NO 25; 74pp; Spanish.

CC The invention relates to a DNA vector (A) for stable transformation and expression of genes (1) in plastids, where (1) is inserted in an artificial intergene region (AIR) formed by combining two 5'-untranslated regions (5'-UTRs) of genes that transcribe in different directions and are derived from plants of different divisions or classes. (A) are used to produce transplastomic angiosperms that have improved agronomic properties (e.g. resistance to biotic or abiotic stress) or express a very wide range of agricultural, veterinary, pharmaceutical, nutritional or industrial products, e.g. enzymes, vaccinating antigens, cytokines or immunoglobulins. Use of (A) eliminates the need for a transposon for gene insertion; inserted genes do not require promoters and terminators; and the structure of flanking sequences in (A) ensures universal applicability. Also any selection marker in (A) can be eliminated by homologous recombination. (A) provides efficient and stable expression of genes without causing any functional alterations. This sequence

CC represents the plasmid pVT1PA-Bar, an example of the vector of the invention.

XX SQ Sequence 6465 BP; 1705 A; 1503 C; 1602 G; 1655 T; 0 U; 0 Other;

Query Match 91.7%; Score 122; DB 12; Length 6465; Best Local Similarity 99.3%; Pred. No. 8; Se-33; Mismatches 0; Indels 1; Gaps 1;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Query Match 91.7%; Score 122; DB 12; Length 6465; Best Local Similarity 99.3%; Pred. No. 8; Se-33; Mismatches 0; Indels 1; Gaps 1;

Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GCTGCCCGCCGCGTGTCAATGAAATGAGGCTGGGATTGACCTGACGGGG 60  
Db 1918 GCTGCCCGCCGCGTGTCAATGAAATGAGGCTGGGATTGACCTGACGGGG 1977

Qy 61 CAGGGATGGCTATA-TCTGGAGGCACTCGGGCATAAGAGGCTTGATACGT 119  
Db 1978 CAGGGATGGCTATA-TCTGGAGGCACTCGGGCATAAGAGGCTTGATACGT 2037

Qy 120 TGTAGGGAGGATT 133  
Db 2038 TGTAGGGAGGATT 2051

RESULT 15

ADM01290 standard; DNA; 6659 BP.

ID ADM01290

AC XX

DT 01-JUL-2004 (first entry)

DE Plasmid pVT1PA-aada DNA sequence.

KW vector; plastid; artificial intergene region; plant; transplastomic angiosperm; agronomic property; stress resistance; rbcl gene; ds.

OS Unidentified.

XX WO2004029256-A2.

XX PD 08-APR-2004.

PP 15-SEP-2003; 2003WO-CU0000009.

PR 27-SEP-2002; 2002CU-00000208.

PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.

PT Selman-Housein Sosa, G., Aguilar Cabeza, E., Gonzalez Quintero ADC;  
PI Ramos Gonzalez O;  
XX DR WPI; 2004-316131/29.

PT DNA vector for transformation and expression in plastids, useful e.g. for producing pharmaceutical proteins or improving agronomic properties, has gene inserted in artificial intergene region.

PS Example 3; SEQ ID NO 22; 74pp; Spanish.

CC The invention relates to a DNA vector (A) for stable transformation and expression of genes (1) in plastids, where (1) is inserted in an artificial intergene region (AIR) formed by combining two 5'-untranslated regions (5'-UTRs) of genes that transcribe in different directions and are derived from plants of different divisions or classes. (A) are used to produce transplastomic angiosperms that have improved agronomic properties (e.g. resistance to biotic or abiotic stress) or express a very wide range of agricultural, veterinary, pharmaceutical, nutritional or industrial products, e.g. enzymes, vaccinating antigens, cytokines or immunoglobulins. Use of (A) eliminates the need for a transposon for gene insertion; inserted genes do not require promoters and terminators; and the structure of flanking sequences in (A) ensures universal applicability. Also any selection marker in (A) can be eliminated by homologous recombination. (A) provides efficient and stable expression of

CC genes without causing any functional alterations. This sequence  
CC represents the plasmid pVTPA-aada, an example of the vector of the  
XX invention.

SQ Sequence 6659 BP; 1790 A; 1490 C; 1636 G; 1743 T; 0 U; 0 Other;  
Query Match 91.7%; Score 122; DB 12; Length 6659;  
Best Local Similarity 99.3%; Pred. No. 8.8e-33;  
Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 GCTCCCCCGCGTCCTCAATGAGATGGTAAAGGGCTGTGGGATTGAGGTGGGG 60  
Db 1918 GCTCCCCCGCGTCCTCAATGAGATGGTAAAGGGCTGTGGGATTGAGGTGGGG 1977  
QY 61 CAGGGATGGTATA-TTCTGGGAGCGACTCCGGCGGAATACGAAAGGCCTGGATACAT 119  
Db 1978 CAGGGATGGTATA-TTCTGGGAGCGAACCTCCGGCGGAATACGAAAGGCCTGGATACAT 2037  
QY 120 TGTAGGGAGGGATT 133  
Db 2038 TGTAGGGAGGGATT 2051

Search completed: April 17, 2006, 23:45:51  
Job time : 487 secs

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OM nucleic - nucleic search, using sw model

Run on: April 17, 2006, 23:37:51 ; Search time 2233 Seconds  
(w/o alignment) 3385.660 Million cell updates/sec

Title: US-10-663-241-32

Perfect score: 133

Sequence: 1 gctcccccggcggttcaa.....tacagtgttagggaggatt 133

Scoring table: IDENTITY\_NTC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenBank:\*

1: gb\_ba:\*

2: gb\_in:\*

3: gb\_env:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pr:\*

9: gb\_ro:\*

10: gb\_sts:\*

11: gb\_sy:\*

12: gb\_un:\*

13: gb\_vl:\*

14: gb\_hmg:\*

15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query %	Match Length	DB ID	Description	
1	133	100.0	133	6 BD106711	BD106711 Plastid P	
2	133	100.0	133	6 AR403658	AR403658 Sequence	
3	122	91.7	176	6 CQ197808	CQ197808 Sequence	
4	122	91.7	1143	6 AR368829	AR368829 Sequence	
5	122	91.7	1148	6 CQ930289	CQ930289 Sequence	
6	122	91.7	1330	6 CQ930287	CQ930287 Sequence	
7	122	91.7	1332	6 CQ930287	CQ930287 Sequence	
8	122	91.7	1336	11 AR061065	AR061065 Plastid t	
9	122	91.7	4126	11 XXU12814	U12814 Transformat	
10	122	91.7	4126	11 XXU12815	U12815 Transformat	
11	122	91.7	4304	11 AX005806	AX005806 Transform	
12	91.7	5834	6 CQ97809	CQ97809 Sequence		
13	91.7	5834	6 CQ97819	CQ97819 Sequence		
14	91.7	6465	6 CQ97816	CQ97816 Sequence		
15	91.7	6659	6 CQ97816	CQ97816 Sequence		
c	16	122	91.7	7454	11 CTR312391	Au312391 Chloroplast
c	17	122	91.7	7549	6 CQ97818	CQ97818 Sequence
c	18	91.7	7626	11 CTR312392	Au312392 Chloroplast	

**ALIGNMENTS**

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
2	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
3	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
4	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
5	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
6	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
7	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
8	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
9	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
10	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
11	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
12	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
13	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
14	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
15	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
16	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
17	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32
18	BD106711	Plastid promoters for transgene expression in the plastids of higher plants.	BD106711	BD106711.1	GI:23201529	JP 2002502262-A/32.		1 (bases 1 to 133)	Maliga,P., Silhavy,D. and Sriraman,P.	Plastid promoters for transgene expression in the plastids of higher plants	RUTGERS THE STATE UNIVERSITY OF NEW JERSEY	PN JP 2002502262-A/32

RESULT 2		ORIGIN	
QY	61 CAGGATGGCTATAATTCTGGAGGCAACTCCGGGGATACGAGCGCTTGATAGTT 120	Query Match	91.7%; Score 122; DB 6; Length 176;
Db	61 CAGGATGGCTATAATTCTGGAGGCAACTCCGGGGATACGAGCGCTTGATAGTT 120	Best Local Similarity	99.3%; Pred. No. 5. 3e-30;
QY	121 GTTGGAGGGATT 133	Matches	0; Mismatches 0; Indels 1; Gaps 1;
Db	121 GTTGGAGGGATT 133	SOURCE	Unknown.
		ORGANISM	Unclassified.
		REFERENCE	1 (bases 1 to 133)
		AUTHORS	Maliga, P., Silhavy, D. and Sriraman, P.
		TITLE	Plastid promoters for transgene expression in the plastids of higher plants
		JOURNAL	Patent: US 6624296-A 32 23-SEP-2003; Rutgers, The State University of New Jersey; East Brunswick, NJ
		FEATURES	Location/Qualifiers
		SOURCE	1. .133 /organism="unknown" /mol_type="genomic DNA"
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Query	Match 100.0%; Score 133; DB 6; Length 133; Best Local Similarity 100.0%; Pred. No. 1e-33; Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	REFERENCE	AR368829/c
Qy	1 GTCGCCCGCCGCTGTCATAGAGATGATAGAGACTCGGGGATAGCTGAGGGG 60	AUTHORS	Maliga, P., Sikdar, S. and Reddy, S. V.
Db	1 GTCGCCCGCCGCTGTCATAGAGATGATAGAGACTCGGGGATAGCTGAGGGG 60	TITLE	Plastid transformation in <i>Arabidopsis thaliana</i>
QY	61 CAGGGATGGCTATAATTCTGGAGGCAACTCCGGGGATACGAGCGCTTGATAGTT 120	JOURNAL	Patent: US 6376744-A 6 23-APR-2002; Rutgers, The State University of New Jersey; New Brunswick, NJ
Db	61 CAGGGATGGCTATAATTCTGGAGGCAACTCCGGGGATACGAGCGCTTGATAGTT 120	FEATURES	Location/Qualifiers
QY	121 GTTGGAGGGATT 133	SOURCE	1. .1143 /organism="unknown" /mol_type="genomic DNA"
RESULT 3		ORIGIN	
Query	Match 91.7%; Score 122; DB 6; Length 1143; Best Local Similarity 99.3%; Pred. No. 5. 9e-30; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	REFERENCE	AR368829
Qy	1 GTCCCCCGGCGCTGTCATAGAGATGATAGAGGTCTGGGATAGCTGAGGGGG 60	AUTHORS	Maliga, P., Sikdar, S. and Reddy, S. V.
Db	1 GTCCCCCGGCGCTGTCATAGAGATGATAGAGGTCTGGGATAGCTGAGGGGG 60	TITLE	Plastid transformation in <i>Arabidopsis thaliana</i>
QY	1130 GTCCCCCGGCGCTGTCATAGAGATGATAGAGGTCTGGGATAGCTGAGGGGG 1071	JOURNAL	Patent: US 6376744-A 6 23-APR-2002; Rutgers, The State University of New Jersey; New Brunswick, NJ
Db	1130 GTCCCCCGGCGCTGTCATAGAGATGATAGAGGTCTGGGATAGCTGAGGGGG 1071	FEATURES	Location/Qualifiers
QY	61 CAGGGATGGCTATAATTCTGGAGGCAACTCCGGGGATACGAGCGCTTGATAGTT 119	SOURCE	1. .1143 /organism="unknown" /mol_type="genomic DNA"
RESULT 4		ORIGIN	
Query	Match 91.7%; Score 122; DB 6; Length 1143; Best Local Similarity 99.3%; Pred. No. 5. 9e-30; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	REFERENCE	AR368829
Qy	1 GTCCCCCGGCGCTGTCATAGAGATGATAGAGGTCTGGGATAGCTGAGGGGG 60	AUTHORS	Maliga, P., Sikdar, S. and Reddy, S. V.
Db	1 GTCCCCCGGCGCTGTCATAGAGATGATAGAGGTCTGGGATAGCTGAGGGGG 60	TITLE	Plastid transformation in <i>Arabidopsis thaliana</i>
QY	1130 GTCCCCCGGCGCTGTCATAGAGATGATAGAGGTCTGGGATAGCTGAGGGGG 1071	JOURNAL	Patent: US 6376744-A 6 23-APR-2002; Rutgers, The State University of New Jersey; New Brunswick, NJ
Db	1130 GTCCCCCGGCGCTGTCATAGAGATGATAGAGGTCTGGGATAGCTGAGGGGG 1071	FEATURES	Location/Qualifiers
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RESULT 5		ORIGIN	
REFERENCE	C0830289	REFERENCE	1 (bases 1 to 1148)
AUTHORS	Tissot, G., Misiewski, J.P. and Ferullo, J.M.	AUTHORS	Tissot, G., Misiewski, J.P. and Ferullo, J.M.
TITLE	Expression of hydroxypyphenylpyruvate dioxygenase in plastids of plants for herbicide tolerance	TITLE	Expression of hydroxypyphenylpyruvate dioxygenase in plastids of plants for herbicide tolerance
JOURNAL	Patent: WO 2004029556-A 14 08-APR-2004; CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CU)	JOURNAL	Patent: WO 2004055191-A 3 01-JUL-2004; Biogemma (FR)
FEATURES		ORGANISM	
SOURCE	1. .176 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref=taxon:32530"	ORGANISM	Other sequences; artificial sequences.
		REFERENCE	1 (bases 1 to 1148)
		AUTHORS	Belman-housein Sosa, G., aguiar Cabeza, E., gonz lez Quintero, A.D. and ramos gonz lez O.
		TITLE	Vector for the production of transplastomic angiosperm plants
		JOURNAL	Patent: WO 2004029556-A 14 08-APR-2004; CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CU)
FEATURES		ORGANISM	
SOURCE	1. .176 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref=taxon:32530"	ORGANISM	Other sequences; artificial sequences.
		REFERENCE	1 (bases 1 to 1148)
		AUTHORS	Tissot, G., Misiewski, J.P. and Ferullo, J.M.
		TITLE	Expression of hydroxypyphenylpyruvate dioxygenase in plastids of plants for herbicide tolerance
		JOURNAL	Patent: WO 2004055191-A 3 01-JUL-2004; Biogemma (FR)

FEATURES source	location/Qualifiers
	1. .1148 /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Synthetic construct"
promoter	1. .117 /note="Prrn" 118. .135 /note="5' rbcL"
5' UTR	
CDS	136. .930 /note="unnamed protein product; aada" /codon_start=1 /transl_table=11 /protein_id="CAH04014.1" /db_xref="GI:50250783" /translation="MDEPAVIAEVSTOLSEVVGVERHLPEPTLAVLYGSAVDGKL PHSDIDLIVVTVRLDETRALDLTASPGSESETAVERVTVRDIDFWRY PAKRLQFGWORLDILAGIPEPATIDAILLTAKREISVALGPAABLFDPVE QDIFEALENITLTMSPPDWAGDERSNVVLTSLRWSAVGKIAPKDVADWAMERLP AQYQPVLEARQVLYQBEDRLASRADOLEBFHVVKGBTIKVVK" terminator 931. .1148 /note="3' rbcL"
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Query Match	91.7%; Score 122; DB 6; Length 1148; Best Local Similarity 99.3%; Pred. No. 5. 9e-30; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Matches	133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy	1 GCTCCCCCGCCGCTGTCATGAGAATGATAGAGGCTCGTGGATTGACCTGAGGGG 60
Db	1 GCTCCCCCGCCGCTGTCATGAGAATGATAGAGGCTCGTGGATTGACCTGAGGGG 60
ORIGIN	
Query Match	91.7%; Score 122; DB 6; Length 1148; Best Local Similarity 99.3%; Pred. No. 5. 9e-30; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Matches	133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy	1 GCTCCCCCGCCGCTGTCATGAGAATGATAGAGGCTCGTGGATTGACCTGAGGGG 60
Db	1 GCTCCCCCGCCGCTGTCATGAGAATGATAGAGGCTCGTGGATTGACCTGAGGGG 60
RESULT 6	
LOCUS	COB28070 1330 bp DNA linear PAT 05-JUL-2004
DEFINITION	Sequence 11 from Patent WO2004051133.
ACCESSION	COB28070
VERSION	COB28070.1 GI:49731589
KEYWORDS	
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	Tisot,G., Wisniewski,J.P. and Ferullo,J.M.
JOURNAL	Expression of hydroxyphenylpyruvate dioxygenase in plastids of plants for herbicide tolerance
FEATURES source	Patent: WO 2004/055191-A 1 01-JUL-2004; Biogemma (FR) Location/Qualifiers
Qy	120 TCTAGGAGGATT 133
Db	121 TCTAGGAGGATT 134
ORIGIN	
Query Match	91.7%; Score 122; DB 6; Length 1330; Best Local Similarity 99.3%; Pred. No. 6e-30; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Matches	133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy	1 GCTCCCCCGCCGCTGTCATGAGAATGATAGAGGCTCGTGGATTGACCTGAGGGG 60
Db	1 GCTCCCCCGCCGCTGTCATGAGAATGATAGAGGCTCGTGGATTGACCTGAGGGG 60
ORIGIN	
Query Match	91.7%; Score 122; DB 6; Length 1330; Best Local Similarity 99.3%; Pred. No. 6e-30; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Matches	133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy	1 GCTCCCCCGCCGCTGTCATGAGAATGATAGAGGCTCGTGGATTGACCTGAGGGG 60
Db	1 GCTCCCCCGCCGCTGTCATGAGAATGATAGAGGCTCGTGGATTGACCTGAGGGG 60
RESULT 8	
LOCUS	AR368830 1417 bp DNA linear PAT 12-SEP-2003
DEFINITION	Sequence 7 from patent US 6376744.
ACCESSION	AR368830

VERSION Am368830.1 GI:34603192  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1. (bases 1 to 1417)  
 AUTHORS Maliga,P., Sikdar,S. and Reddy,S.V.  
 TITLE Plastid transformation in *Arabidopsis thaliana*  
 JOURNAL Patent: US 6316744-A 7 Mar 2002;  
 Rutgers, The State University of New Jersey; New Brunswick, NJ  
 FEATURES source Location/Qualifiers  
 1. 1417  
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 Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 GCTCCCCCGCGTCGTCAATGAGAATGGCTCTGGGTTGACGTAGGGGG 60  
 Db 23 GCTCCCGCCGCGTCGTCAATGAGAATGGCTCTGGGTTGACGTAGGGGG 82  
 QY 61 CAGGGATGGCTATAATCTGGAGGCAACTCGGCGGAATAGAAGCGCTGGATTAGACT 119  
 Db 83 CAGGGATGGCTATAATCTGGAGGCAACTCGGCGGAATAGAAGCGCTGGATTAGACT 142  
 QY 120 TGTAGGGAGGATT 133  
 Db 143 TGTAGGGAGGATT 156  
 RESULT 9  
 AF061065/c Locus AF061065 Definition plastid transformation vector ps331A 3136 bp DNA linear SYN 14-NOV-1998  
 ACCESSION AF061065  
 VERSION AF061065.1  
 KEYWORDS SOURCE plastid transformation vector ps331A  
 ORGANISM other Sequences; artificial sequences; vectors.  
 REFERENCE AUTHORS 1. (bases 1 to 3136)  
 Syrab,Z. and Maliga,P.  
 TITLE High-frequency plastid transformation in tobacco by selection for a chimeric aada gene. Proc. Natl. Acad. Sci. U.S.A. 90 (3), 913-917 (1993)  
 JOURNAL PUBMED REFERENCE 8381537  
 AUTHORS Sikdar,S.R., Serino,G., Chaudhuri,S. and Maliga,P.  
 TITLE JOURNAL REFERENCE 2 (bases 1 to 3136)  
 AUTHORS Serino,G. and Maliga,P.  
 TITLE JOURNAL REFERENCE 3 (bases 1 to 3136)  
 AUTHORS Direct submission  
 JOURNAL Submitted (22-APR-1998) Wakeman Institute, Rutgers University, 190 Frelinghuysen Road, Piscataway, NJ 08854-8020, USA  
 FEATURES source Location/Qualifiers  
 1. 3136  
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 1. 1058  
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 complement (831..902)  
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 complement(1262..2053)  
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 promoter complement(2054..2188)  
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 Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 1 GCTCCCCCGCGTCGTCAATGAGAATGGCTCTGGGTTGACGTAGGGGG 60  
 Db 2188 GCTCCCCCGCGTCGTCAATGAGAATGGCTCTGGGTTGACGTAGGGGG 2129  
 QY 61 CAGGGATGGCTATAATCTGGAGGCAACTCGGCGGAATAGAAGCGCTGGATTAGACT 119  
 Db 2128 CAGGGATGGCTATAATCTGGAGGCAACTCGGCGGAATAGAAGCGCTGGATTAGACT 2069  
 QY 120 TGTAGGGAGGATT 133  
 Db 2068 TGTAGGGAGGATT 2055  
 RESULT 10  
 XXU12814/c Locus XXU12814 Definition Transformation vector PPRV112A, plastid targeting segment.  
 ACCESSION UI12814  
 VERSION UI12814.1  
 KEYWORDS SOURCE Cloning vector PPRV112A  
 ORGANISM Cloning vector PPRV112A  
 other Sequences; artificial sequences; vectors.  
 REFERENCE AUTHORS 1. (bases 1 to 426)  
 Zoubenko,O.V., Allison,L.A., Syrab,Z. and Maliga,P.  
 TITLE TITLE Efficient targeting of foreign genes into the tobacco plastid genome  
 JOURNAL Nucleic Acids Res. 22 (19), 3819-3824 (1994)  
 PUBMED REFERENCE 7937099  
 AUTHORS Hajdukiewicz,P.T.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-1994) Peter T. Hajdukiewicz, Wakeman Inst., Rutgers University, Old Hoes Lane, Piscataway, NJ 08855, USA  
 FEATURES source  
 1..4126  
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AUTHORS Suzuki, J Y. and Maliga, P.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-JUL-2000) Waksman Institute, Rutgers University, 190  
 Frelinghuysen Road, Piscataway, NJ 08854, USA  
 FEATURES Location/Qualifiers  
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 /mol\_type="genomic DNA"  
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 Best Local Similarity 99.3%; Pred. No. 6.4e-30;  
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 3' UTR  
 gene  
 mRNA  
 CDS  
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 DEFINITION Sequence 15 from Patent WO2004029256.  
 ACCESSION CQ797809  
 VERSION CQ797809.1 GI:46426082  
 KEYWORDS synthetic construct  
 SOURCE  
 ORGANISM synthetic construct  
 REFERENCE other sequences; artificial sequences.

**AUTHORS** selman-housein Sosa, G., aguiar Cabaza,E., gonz lez Quintero,A.D.  
**TITLE** Vector for the production of transplastomic angiosperm plants  
**JOURNAL** Patent: WO 2004029256-A 15 08-APR-2004;  
**CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CU)**  
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**Query Match** 91.7%; Score 122; DB 6; Length 6659; Best Local Similarity 99.3%; Pred. No. 6. 5e-30; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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**Db** 1918 GCTCCCCCGCCGCTGGTCAATGAGAATGGATAAGAGGTCTGGATTGACGTGAGGGGG 1977

**QY** 61 CAGGGATGGCTATA-TTCGGGAGGGAATCTCGGGCGATATCGAAAGCCTTGATGAGT 119  
**Db** 1978 CAGGGATGGCTATA-TTCGGGAGGGAATCTCGGGCGATATCGAAAGCCTTGATGAGT 2037

**QY** 120 TGTAGGAGGGATT 133  
**Db** 2038 TGTAGGAGGGATT 2051

**RESULT 14**

**LOCUS** CQ797819 6465 bp DNA  
**DEFINITION** Sequence 25 from Patent WO2004029256.  
**ACCESSION** CQ797819  
**VERSION** CQ797819.1  
**KEYWORDS** synthetic construct  
**SOURCE** synthetic construct  
**ORGANISM** other sequences; artificial sequences.  
**REFERENCE**  
**AUTHORS** selman-housein Sosa, G., aguiar Cabeza, E., gonz lez Quintero,A.D.  
**TITLE** Vector for the production of transplastomic angiosperm plants  
**JOURNAL** Patent: WO 2004029256-A 22 08-APR-2004;  
**CENTRO DE INGENIERIA GENETICA Y BIOTECNOLOGIA (CU)**  
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**ORIGIN**

**Query Match** 91.7%; Score 122; DB 6; Length 6659; Best Local Similarity 99.3%; Pred. No. 6. 5e-30; Matches 133; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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**QY** 61 CAGGGATGGCTATA-TTCGGGAGGGAATCTCGGGCGATATCGAAAGCCTTGATGAGT 119  
**Db** 1978 CAGGGATGGCTATA-TTCGGGAGGGAATCTCGGGCGATATCGAAAGCCTTGATGAGT 2037

**QY** 120 TGTAGGAGGGATT 133  
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**SEARCH**

Search completed: April 18, 2006, 00:23:15  
 Job time : 2235 secs

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**ORIGIN**

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**QY** 61 CAGGGATGGCTATA-TTCGGGAGGGAATCTCGGGCGATATCGAAAGCCTTGATGAGT 119  
**Db** 1978 CAGGGATGGCTATA-TTCGGGAGGGAATCTCGGGCGATATCGAAAGCCTTGATGAGT 2037

**QY** 120 TGTAGGAGGGATT 133  
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